Connecting via Winsock to STN

0+ FILE CAPACUS	FILE	0+ FILE BIOENG 0+ FILE BIOTECHABS 0+ FILE BIOTECHABS	BILE BILE BILE	UN FILE ADISCTI ON FILE ADISINSIGHT ON FILE ADISHWS ON FILE ACCOUNT ON	74 FILES IN THE FILE LIST IN STNINDEX Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0° with SET DETAIL OFF.	INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, AQUALINE, ANABSTR, ANTE, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHASS, BIOTECHOS, BIOTECHOO, CABA, CANCERLIT, CAPLUS, CEABA-VITB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DGENE,' ENTERED AT 12:34:53 ON 07 OCT 2004	=> index biosci FILE 'DRUGMONG' ACCESS NOT AUTHORIZED COST IN U.S. DOLLARS ENTRY SESSION FULL ESTIMATED COST 1067.98 1068.19	COST IN U.S. DOLLARS SINCE FILE TOTAL ENTRY SESSION FULL ESTIMATED COST 1067.56 1067.77	PASSWORD: * * * * * RECONNECTED TO STN INTERNATIONAL * * * * * * \$10.0 RESIMED IN FILE 'REGISTRY' AT 12:34:32 ON 07 OCT 2004 FILE 'REGISTRY' ENTERED AT 12:34:32 ON 07 OCT 2004 COPYRIGHT (C) 2004 American Chemical Society (ACS)	Welcome to STN International! Enter x:x LOGINID:SSSPTA1653RAW
1 1 1	FILE 'B	FILE 'B	FILE 'B	FILE 'A	FILE 'A	'SQSP'	FILE 'AI	FILE 'A	SET COM => s l1 FILE 'AI 'SQSP' :	set o

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FILE CEN

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FILE 'BIOSIS'
                                                                            'BIOCOMMERCE'
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O CIPRINOGESTY] [ANDOEGILMEPSTYV] [EGKSY] [PDENOGLKSTY] [RGW] [LIKOMOPS
O VJ. [ILFWY]/SQSP
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IS NOT A VALID FIELD CODE
O C(PRNDOGFSTY) [ANDQEGILMFPSTYV] [EGKSY] [PDENQGLKSTY] [RGW] [LIKONQPS
TV] [ILFWY]/SQSP
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IS NOT A VALID FIELD CODE
O C[PRUDGESTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIKMNQPS
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O C(PRNDQGFSTY) [ANDQEGILMFPSTYV] [EGKSY] [PDENQGLKSTY] (RGW] [LIMMQPS
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O C(PRNDQGFSTY) [ANDQEGILMFPSTYV] [EGKSY] (PDENQGLKSTY) [RGW] [LIMMQPS
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'IS NOT A VALID FIELD CODE
O C[PRNDQGFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIRONQPS
TV][ILFWY]/SQSP
'BIOBUSINESS'
'IS NOT A VALID FIELD CODE
O C[PRNDQGFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIRONQPS
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IS NOT A VALID FIELD CODE
O C[PRNDQGESTY] [ANDQEGILMFPSTYV] [EGKSY] [PDENQGLKSTY] [RGW] [LIRONQPS
TV] [LIFWY]/SQSP
AGRICOLA'
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O C[PRNDQGFSTY] [ANDQEGILMFPSTYV] [EGKSY] [PDENQGLKSTY] [RGW] [LIRONQPS
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O C[PRNDQGFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIKMNQPS
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O C(PRNDQGFSTY)[ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIKMNQPS
TV][ILFWY]/SQSP
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FILE CROPB
FILE CROPU
FILE DISSABS
FILE DDFB
FILE DDFU
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FILE 'CROPB'
'SQSP' IS NOT FILE 'CONFSCI'
'SQSP' IS NOT A VALID FIELD CODE
O C[PRUDQGFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIKONQPS FILE 'CEN'
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'SQSP' IS NOT A VALID FIELD CODE
TV] [LICANQESTY] [ANDQEGILMEPSTYV] [EGKSY] [PDENQGLKSTY] [RGW] [LICANQPS
TV] [ILEWY] / SQSP FILE 'CABA' FILE 'CIN'
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(SQSP' IS NOT A VALID FIELD CODE
TV] [ANDQEGILMFPSTYV] [EGKSY] [PDENQGLKSTY] [RGW] [LIKANQPS
TV] [ILFWY] / SQSP FILE 'DDFB'
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O C[PRNDQGFSTY] [ANDQEGILMFPSTYY] [EGKSY] [PDENQGLKSTY] [RGW] [LIKYNQPS
TV] [ILFWY] /SQSP FILE 'DISSABS' FILE 'CROPU' 'SQSP' IS NOT A VALID FIELD CODE

O C[PRNDQGFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIKMNQPS
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TV] [ILFWY] /SQSP IS NOT A VALID FIELD CODE

0 C[PRNDQGFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIMMQPS
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TV] [ILFWY] / SQSP IS NOT A VALID FIELD CODE

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O C[PRNDQGFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIKMMQPS TV][ILFWY]/SQSP

FILE 'DDEU'
'SQSP' IS NOT A VALID FIELD CODE
O C[PRNDQEFSTY][ANDQEGILMFPSTYV][EGKSY][PDENQGLKSTY][RGW][LIMMNQPS
TV][ILFWY]/SQSP

SEARCH NOT VALID, USE RUN GETSEQ

=> file home]
'HOME|' IS NOT A VALID FILE NAME
SESSION CONTINUES IN INDEX FILES 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA,

AQUALINE, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOTECHABS, BANABSTR, ANTE, AQUASCI, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONTSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, IMSDRUGMS, DRUGU, IMSRESEARCH, EMBAL, EMBASE, ESBIOBASE, FEDRIP, FORMAD, FORECE, FROSTI, FSTA, GENBANK, HELLSAFE, IFIPAT, IMSPRODUCT, JICST-EPLUS, KOSMET, LIFESCI, MEDICONF, MEDILINE, NOSHTIC, NITS, NUTRACEUT, OCEAN, PASCAL, PCTGEN, PHAR, PHARMAMI, PHIC, PHIN, PROMT, PROUSDDR, RDISCLOSURE, SCISEARCH, SYNTHLINE, TOXCENTER, USPATFULL, USPATZ, VETB, VETU, WATER, WPIDS, WPIFY, WPIFW, WILL, USPATZ, VETB, VETU, WATER, WPIDS, WPIFY, WPIFY, WPIENDEX' Enter "HELP FILE NAMES" at an arrow prompt (-9) for a list of files that are available. If you have requested multiple files, you can specify a corrected file name or you can enter "IGNORE" to continue accessing the remaining file names entered.

=> file home COST IN U.S. DOLLARS FULL ESTIMATED COST SINCE FILE ENTRY 1.71 TOTAL SESSION 1069.90

FILE 'HOME' ENTERED AT 12:36:28 ON 07 OCT 2004

=> log h
COST IN U.S. DOLLARS FULL ESTIMATED COST SINCE FILE ENTRY 0.21 TOTAL SESSION 1070.11

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 12:36:41 ON 07 OCT 2004

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID: SSSPTA1653RAW

PASSWORD:

* * * * * RECONNECTED TO STN INTERNATIONAL * * * * * *
SESSION RESUMED IN FILE 'HOME' AT 12:38:07 ON 07 OCT 2004

COST IN U.S. DOLLARS

SINCE FILE TOTAL SESSION

SESSION RESUMED IN FILE 'BIOSIS, CAPLUS' AT 12:40:39 ON 07 OCT 2004 FILE 'BIOSIS, CAPLUS' AT 12:40:39 ON 07 OCT 2004 PRILE 'BIOSIS' ENTERED AT 12:40:39 ON 07 OCT 2004 COPYRIGHT (C) 2004 The Thomeson Corporation. FILE 'CAPLUS' ENTERED AT 12:40:39 ON 07 OCT 2004 COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS) FILE 'CAPLUS' ENTERED AT 12:38:20 ON 07 OCT 2004
USE IS SUBJECT TO THE TERMS OF YOR SIN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USACETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS) FILE 'BIOSIS' ENTERED AT 12:38:20 ON 07 OCT 2004 Copyright (c) 2004 The Thomson Corporation. SESSION WILL BE HELD FOR 60 MINUTES STN INTERNATIONAL SESSION SUSPENDED AT 12:38:57 ON 07 OCT 2004 "> s 11
"SQSP" IS NOT A VALID FIELD CODE
"SQSP" IS NOT A VALID FIELD CODE FULL ESTIMATED COST => file biosis caplus
COST IN U.S. DOLLARS => file home COST IN U.S. DOLLARS Connecting via Winsock to STN FULL ESTIMATED COST => log h
COST IN U.S. DOLLARS FULL ESTIMATED COST FULL ESTIMATED COST Welcome to STN International! Enter x:x COST IN U.S. DOLLARS LOGINID: SSSPTA1653RAW 0 L1 SINCE FILE ENTRY 1.29 SINCE FILE SINCE FILE SINCE FILE ENTRY 1.29 ENTRY 0.21 ENTRY 1.29 0.21 TOTAL SESSION 1070.11 TOTAL SESSION 1071.40 TOTAL SESSION 1071.40 TOTAL SESSION 1071.40 1070.11

FILE 'HOME' ENTERED AT 12:40:48 ON 07 OCT 2004

=> e wescott/in

1114

FULL ESTIMATED COST

PROCESSING IS APPROXIMATELY 2
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PROCESSING COMPLETED FOR L45 Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the American Chemical Society and is provided to assist you in searching databases on SIN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is strictly prohibited. FILE 'CAPLUS' ENTERED AT 12:40:52 ON 07 OCT 2004 USE IS SUBJECT TO THE TERMS OF YOUR STON OUTOMER AGREEMENT. PLEASE SEE "HELD USACETERMS" FOR DETAILS. COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS) FILE COVERS 1907 - 7 Oct 2004 VOL 141 ISS 15 FILE LAST UPDATED: 6 Oct 2004 (20041006/ED) FULL ESTIMATED COST COST IN U.S. DOLLARS L48 => s 142 or 143 or 144 L45 5029 L42 OR L43 OR L44 L43 L42 147 L46 => s 13 => s 12 => s 11 => s 148 not wescott/au => s 146 not wescott/in This file contains CAS Registry Numbers for easy and accurate substance identification. 0 WESCOTT/AU 4761 L48 NOT WESCOTT/AU 0 WESCOTT/IN 4761 L47 NOT WESCOTT/IN 4761 S L46 5026 L1 4761 DUP REM L45 114 L2 œ 20% COMPLETE FOR L45
42% COMPLETE FOR L45
65% COMPLETE FOR L45
87% COMPLETE FOR L45 (268 DUPLICATES REMOVED) SINCE ENTRY 0.21 TOTAL SESSION 1071.61

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        'HOME' ENTERED AT 12:00:59 ON 07 OCT 2004)
10 S C(PROGESTY) [ANDQEGILINEPSTYV) [EGISY] [PDENGGINSTY] [RM] [LIM
57 S C(PROGESTY) [ANDQEGILINEPSTYV) [ES] [PDENGSTY] W[LIMAGSTV] [RM]
58 S (CPROGESTY) [ANDQEGILINEPSTYVY] [ES] [PDENGSTY] W[LIMAGSTV] [RM]
59 S (CPROGEDILINEPSTWYV] [ANGGILINEPT] C(PRNDGGILINEPSTYVY) [
60 S W[ANDQEGILINEPSTWYV] [ANGGILINEPT] C(PRNDGGILINEPSTWYV] [
61 S W[ANDQEGILINEPSTWYV] [ANGGILINEPT] C(PRNDGGILINEPSTWYV] [
61 S W[ANDQEGILINEPSTWYV] [ANGGILINEPT] C(PRNDGGILINEPSTWYV] [
62 S W[ANGLIM] [ALMP] CP [DEGMM] E [PDENS] [LT] FCW [DGHES] [AGHES] /SOSP [
63 S CYS-SER-ASP-CLU-SER-TRP-LEU-TRP-CYS' /SOSP [
64 S CYS-PRO-MET-SER-GLU-TRP-LEU-TRP-CYS' /SOSP [
65 S CYS-SER-ASP-CLU-SER-TRP-THR-PHE-CYS' /SOSP [
65 S CYS-SEN-CLY-CLU-PRO-TRP-LEU-PHE-CYS' /SOSP [
65 S CYS-SEN-CLY-CLU-PRO-TRP-LEU-PHE-CYS' /SOSP [
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65 S CYS-SEN-CLY-TRP-CLU-PRO-TRP-THR-PHE-CYS' /SOSP [
65 S CYS-SEN-CLY-CLU-PRO-TRP-THR-PHE-CYS' /SOSP [
65 S CYS-SEN-CLY-TYS-ARG-GIN-PHE-CYS' /SOSP [
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65 S CYS-SHO-CLY-CLU-SER-TRR-PHO-LEU-TRP-CYS-TRP-SER-ALA [
65 TRP-MIT-MET-CYS-SER-ALA [
65 TRP-MIT-MET-CYS-TRR-PHO-SHO-SHO-CYS-TRR-ASP-CHY -LLU-PHE-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-MA-LIN-CYS-TRP-MIT-M
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WESCOTT GHARLES R/IN
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129
13 'TRP-GIN-ALA-CYS-GIN-LEU-GLY-TYR-ARG-THR-TYR-CYS-TRP-ASP-GLY
130
13 'TRP-LYS-PHE-CYS-ASP-GLY-GENO-TRP-LEU-PHE-CYS-TRP-ASP-GLY
131
14 'TRP-ASS-GLY-CYS-GLY-TRP-GLY-SER-TRP-LYS-PHE-CYS-GLY-GLU-GLY
132
15 'TRP-LEU-ASN-CYS-GLY-TRP-GLY-SER-GLY-LYS-LEU-CYS-LEU-GLY-VAL
133
16 'TRP-HIS-PHE-CYS-PRO-GLY-GLU-PRO-TRP-HR-PHE-CYS-TRP-ASP-ASP
134
17 'TRP-HIS-PHE-CYS-PRO-GLY-GLU-PRO-TRP-HR-PHE-CYS-TRP-ASP-GLY
135
18 'TRP-GLN-THR-CYS-PRO-GLY-TYR-LEU-ARG-SER-LEU-CYS-TRP-ASP-GLY
136
19 'TRP-GLN-THR-CYS-PRO-GLY-GLU-PRO-TRP-BER-CYS-PRO-ASP-GLY
137
11 S'TRP-GLN-PRO-CYS-PRO-GLY-GLU-PRO-TRP-BC-CYS-TRP-ASP-GLY
138
12 'TRP-GLN-ALA-CYS-PRO-GLY-GLU-SER-TRP-PRO-TYS-TRP-ASP-ARG
139
13 'TRP-GLN-ALA-CYS-PRO-GLY-TYR-LYS-ARG-GLN-PHE-CYS-TRP-ASP-ARG
139
14 'TRP-GLN-ALA-CYS-PRO-GLY-TYR-LYS-ARG-GLN-PHE-CYS-TRP-ASP-ARG
139
15 'TRP-GLN-ALA-CYS-PRO-GLY-TYR-LYS-ARG-GLN-PHE-CYS-TRP-ASP-ARG
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15 'TRP-GLN-ALA-CYS-PRO-GLY-TYR-LYS-ARG-GLN-PHE-CYS-TRP-ASP-ARG
139
15 'TRP-GLN-ALA-CYS-PHE-GLN-LYS-ARG-GLN-PHE-CYS-TRP-ASP-ARG
130
15 'TRP-GLN-ALA-CYS
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INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, AQUALINE, ANABSTR, ANTE, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHABS, BIOTECHAS, BIOTECHAS, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDEB, DDFU, DGENE, ...' ENTERED AT 12:34:53 ON 07 OCT 2004

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L53 6 L44 NOT "WESCOTT CHARLES R"/IN
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151
152
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                                                                    Binding peptides for the KDR receptor and vascular endothelial growth factor/KDR complex and their use in diagnosis, therapy, and imaging of
                                                                                                                 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2004 ACS 2004:634089 CAPLUS
                                                                                                                                                                                                                                                                                                                                                                                                                            FILE
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C., Arbogast, Christophe, Bussat, Philippe, Fan, Hong, Khurana, Sudha;
Linder, Karen E.; Marinelli, Edmund R.; Nanjappan, Palaniappa, Num,
Adrian; Pillai, Radhakrishna; Pochon, Sibylle; Ramalingam, Kondareddiar;
                                         angiogenesis-related disorders
Sato, Aaron K.; Sexton, Daniel J.; Dransfield, Daniel T.; Ladner, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE 'HOME' ENTERED AT 12:36:28 ON 07 OCT 2004
                                                                                                    41:167846
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8 S L3
8 S L3
5029 S L42 OR L43 OR L44
4761 DUP REM L45 (268 DUPLICATES REMOVED)
4761 S L46
4761 S L46 NOT WESCOTT/IN
4761 S L48 NOT WESCOTT/AU
E WESCOTT/IN
4761 S L46 NOT E6
4759 S L46 NOT E6
4759 S L46 NOT E6
4757 S L51 NOT FIBRIN
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FILE CROPB
FILE CROPU
FILE DISSABS
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FILE CEN
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FILE BIOTECHNO
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PRAI US 2002-360851P US 2003-440411P US 2003-382082 WO 2003-US6731 ΡŢ LA English FAN. CNT 2 ξä SO SO WO 2004065621 Shrivastava, Ajay; Song, Bo; Swenson, Rolf E.; Von Wronski, Mathew A. Dyax Corp., USA; Bracco International B.V. PCT Int. Appl., 470 pp. CODEN: PIXXD2 ĕ PATENT NO. 2003074005 RW. ٤ RW: 8 2 4 4 5 5 5 6 5 HR, CR, TR, TR, CY, OM, PT, 3 G G G G NE, NE, NE, A2 TIND TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOT SI, SK, SC, ME, DE, SN, DR MZ, SD,
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The present invention provides peptides, peptide dimers, and multimeric complexes comprising at least one binding moiety for KDR receptor or vascular endothelial growth factor (VEGF)KDR complex, which have a variety of uses wherever treating, detecting, isolating, or localizing angiogenesis is advantageous. Particularly disclosed are synthetic, isolated peptides capable of binding KDR or VEGF/KDR complex with high ascincts, e.g., ranging a KD < 1 mu, M), and dimer and multimeric constructs comprising these polypeptides. The involvement of VEGF and KDR in angiogenesis makes the binding peptides particularly useful for imaging important sites of angiogenesis, e.g., neoplastic tumors, for targeting substances, e.g., therapeutics, including radiotherapeutics, to such sites, and for treating certain disease states, including those assocd.

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L53ANSWER 2 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN PRAI US 2002-360551P P 20020301

US 2003-440411P P 2003013

US 2003-382082 A2 20030303

WO 2003-US6731 A2 2003003

The present invention relates to polypeptides useful for detecting and targeting primary receptors on endothelial cells for VEGF, i.e., VEGF receptor 2, also known as kinase domain region (KDR) and fetal liver kinase-1 (Flk-1), and for imaging and targeting complexes formed by VEGF and KDR. The involvement of VEGF and KDR in angiogenesis makes the VEGF/KDR and KDR binding polypeptides of the present invention particularly useful for imaging important sites of angiogenesis. Ħ ij LA English FAN.CNT 2 ξ PA SO 무급무용 WO 2003074005 KDR and VEGF/KDR binding peptides and their use in diagnosis and therapy Sato, Aaron K.; Sexton, Daniel J.; Ladner, Robert C.; Dransfield, Daniel T.; Swenson, Rolf E.; Marinelli, Edmund R.; Ramalingam, Kondareddiar; Nunn, Adrian D.; Von Wronski, Mathew A.; Shrivastava, Ajay; Pochon, Sibylle; Busset, Philippe; Arbogast, Christophe; Pillai, Radhakrishna; Fan, Hong; Linder, Karen E.; Song, Bo; Nanjappan, Palaniappa Fan, USA; Bracco International B.V.; et al. Š PATENT NO. Patent PCT Int. Appl CODEN: PIXXD2 2003:719271 .39:265740 2004065621 ٤ \$899888598 4067454666 MAC GREEN CON AG CAPLUS MR CE KIT PH CAL # B C E H U B U L U L U L 350 pp. AZ
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US 2003109690 A1 20030612 US 2002-106698 20020327

PRAI US 1999-157137P P 1999029

US 1999-163280P P 19991103

WO 2000-US26524 A2 20000928

US 2002-106698 A 2020327

AB The present invention relates to 8354 novel colon- or colon cancer-related T1 PN 153 LA English FAN.CNT 3 F Di SO ANSWER 3 OF 6 2003:464737 CA 139:2147 disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polymucleotides and polypeptides of the invention. The present invention further relates to methods and/or compas, for inhibiting the productions and/or compass, for inhibiting the productions of the production of the prod cancer-assocd. polypeptides. Novel colon or colon cancer polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human colon- or colon cancer-assocd, polymucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic polymucleotides and the polypeptides encoded by these polymucleotides herein collectively known as "colon or colon cancer antigens," and the use of such colon or colon cancer antigens for detecting disorders of the colon, particularly the presence of colon cancer and colon cancer metastases. More specifically, isolated colon- or colon cancer-assocd. nucleic acid mols. are provided encoding novel colon- or colon US 2003109690 WO 2001022920 function of the polypeptides of the present invention. [This abstracecord is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication U.S. Pat. Appl. Publ., 174 pp., Cont.-in-part of Appl. No. PCT/US00/26524. and their diagnostic and therapeutic applications
Ruben, Steven M.; Barash, Steve C.; Birse, Charles E.; Rosen, Craig A.
Human Genome Sciences, Inc., USA polypeptides. The invention further relates to diagnostic and uncompethods useful for diagnosing, treating, preventing and/or prognosing PATENT NO. Patent Human colon and colon cancer-associated polynucleotides and polypeptides CODEN: USXXCO CAPLUS CAPLUS COPYRIGHT 2004 ACS on OR RESERVED , GB, GR, , GN, GW, 20030612 20010405 AU, AZ, DM, DZ, JP, KE, MK, MN, 20030612 US 2002-106698 WO 2000-US26524 APPLICATION NO. TG AT 유무도요 , BE, CH, SE, BF, CA, CH, GH, GM, LR, LS, PT, RO, US, UZ, DATE 20020327 20000928 집 £2559

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neoplastic tumors, for targeting substances, e.g., therapeutics, including radiotherapeutics, to such sites, and for treating certain disease states, including those assocd. with inappropriate anglogenesis. Disclosed are synthetic, isolated polypeptides capable of binding KDR or VEGF/KDR complex with high affinity (e.g., having a KDK1 .mu.M).

47.6

Nucleic acids and their encoded polypeptides from human nervous system

PRAI US 2000-PV179065

US 2000-PV186626

US 2000-PV186350

US 2000-PV189874

US 2000-PV198123

US 2000-PV29467

US 2000-PV21686

US 2000-PV21686

US 2000-PV216869

US 2000-PV21687

US 2000-PV217487

US 2000-PV217487 B PΙ 닭닭 SO PA polynucleotides, the polypeptides encoded by these polynucleotides herein collectively referred to as "nervous system antigens", and antibodies that immunospecifically bind these polypeptides, and the use of such nervous system polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the nervous system system, including, but not limited to, the presence of nervous system cancer and nervous system metastases. More specifically, 3324 isolated nervous system cDNA mols. and 7200 genomic DNA mols. are provided encoding novel W: AE, AG, AI RW: Rosen, Craig A.; Barash, Stev Human Genome Sciences, Inc., PCT Int. Appl., 1701 pp. CODEN: PIXXD2 The present invention relates to novel nervous system-elated PATENT NO. English Patent BY, S S E G & BE G SL G E2844644 20000302 20000316 20000317 200000726 20000814 20000630 20000204 20000814 20000726 20000714 20000711 20000711 20000707 20000628 20000607 20000519 20000418 Steven C.; Ruben, Steven M. 20010816
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promoting the prodm. and/or function of the polypeptides of the invention. [This abstr. record is two of three records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

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US 2003109690 Al 20030612 US 2002-106698 20020327

US 1999-163280P P 19991103

WO 2000-US26524 W 20000928

US 2002-106698 A 20020327

AB This invention relates to newly identified colon or colon cancer related polymucleotides and the polympatides encoded by these polymucleotides polymucleotides and the polympatides encoded by these polymucleotides of the polympatides of the colon, particularly detecting, preventing and treating disorders of the colon, particularly the presence of colon cancer and close disorders metastases. This invention relates to colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and the recombinant or synthetic methods for producing the same. Also provided are diagnostic methods for producing the same. Also provided are diagnostic
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screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to inhibiting the prodn. and function of the polypeptides of the present
                                                                                                                disorders related to the colon, including colon cancer, and therapsutic methods for treating such disorders. The invention further relates to
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Human Genome Sciences, Inc., USA
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                                                                                                                                                                                     methods for diagnosing and treating, preventing and/or prognosing
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human nervous system polypeptides. Novel nervous system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human nervous system polymucleotides, polypeptides, and/or antibodies. The invention further relates to diagnostic and therapeutic

methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the nervous system, including nervous system cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and

antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compns. for inhibiting or

the wild-type products of these genes function in a common signaling pathway to initiate sperm activation. We have identified the spe-29 gene, which is expressed specifically in the sperm-producing germ line and is predicted to encode a small, novel transmembrane protein.

RE.ONT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD SON 11 P P 56 => s 155 not 153 L56 16 L55 NOT L53 A F P B So AU CS L55 => s 154 L54 검모본 => d 156 bib ab 1-16 ₩ ₩ failure in spermatid activation. Intriguingly, mutant hermaphrodites form functional spermatozoa and become self-fertile upon mating, suggesting that spermatids can be activated by male seminal fluid. Here we describe a mutation in a 4th gene, spe-29, which mimics the phenotype of spe-8, spe-12, and spe-27 mutants. Spe-29 sperm are defective in the initiation C. elegans spermatids complete a dramatic morphogenesis to crawling spermatozoa in the absence of an actin- or tubulin-based cytoskeleton and without synthesizing new gene products. Mutations in 3 genes (spe-8, spe-12, and spe-27) prevent the initiation of this morphogenesis, termed activation. Males with mutations in any of these genes are fertile. By Spe-29 encodes a small predicted membrane protein required for the initiation of sperm activation in Caenorhabditis elegans Nance, Jeremy, Davis, Elizabeth B., Ward, Samuel Department of Molecular and Cellular Biology, University of Arizona, Tucson, AZ, 85721, USA 143 La Jolla Cancer Research Foundation, USA
U.S. 80 pp., Cont.-in-part of U.S. Ser. No. 919,951, abandoned CODEN: USXXAM ANSWER 1 OF 16 CAPLUS COPYRIGHT 2004 ACS on 1999:125754 CAPLUS complete the morphogenetic rearrangements that follow. Mutant alleles of spe-12, spe-27, and spe-29 exhibit genetic interactions that suggest that Genetics (2000), 156(4), 1623-CODEN: GENTAE; ISSN: 0016-6731 Nucleic acids encoding human merosin, merosin fragments and uses thereof of hermaphrodite sperm activation, yet they maintain the ability to 2001:35512 CAPLUS 134:249803 Engvall, Eva; Leivo, Ilmo and merosin enhancement of neurite growth contrast, mutant hermaphrodites are self-sterile when unmated due to a English Genetics Society of America 30:178389 .54 and py<1999 18927350 PY<1999 16 L54 AND PY<1999 Journal not e6 5 "WESCOTT CHARLES R"/IN 112 L43 NOT "WESCOTT CHARLES R"/IN ALL CITATIONS AVAILABLE IN THE RE FORMAT 156(4), 1623-1633 STN

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24	and for certain diagnostic applications.	invention further pro	provided. The human	expression of recombinant proteins by use of a	antibodies, vectors f	nucleic acid mols. wh	designated merosin (a	of a protein, the pro	This invention provides an	WO 1994-US10730	US 1993-125077	US 1991-734201		US 1990-472319	US 5837496		JP 09505985	CH, DE,	EP 720651	AU 9478770	CF,	-	KZ, LK, LV,	W: AM, AU, BB, B		WO 9508628	CA 2172385	US 5872231	 PATENT NO. K	FAN.CNT 3	91111111
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FOR THIS	ns,	invention further provides the use of merosin to promote neurite growth		use of a host vector system	nt prodn. of merosin, and	nucleic acid mols. which encode merosin fragments. Anti-merosin	designated merosin (also known as laminin 2). Also provided are	protein, the protein having an apparent mol. wt. of about 800 kDa,	nucleic acid mol. encoding						US 1995-460309	US 1995-393250	JP 1995-509932	LI, NL, SE	EP 1994-929860	AU 1994-78770	N, MI, MR, NE, SN, TD,	GR, IE, IT, LU,	PL, RO, RU, SD,	N, CZ, FI, GE, HU, JP,		WO 1994-US10730	CA 1994-2172385	US 1993-125077	APPLICATION NO.		
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SO Allele frequencies of the STR locus HumFGA in an Italian population Busceni, L.; Tagliabracoi, A.; Bianchi, F.; Paoli, M.; Sassaroil, C.; Rodriguez, D.; Caenazzo, L.; Penzano, E.; Cortivo, P.; Previdere, C.; Peloso, G.; Pierucci, G.; Bibbiani, R.; Nardone, M.; Spinetti, I.; University of Ancona, Domenici, R.; Bargagna, M. International Congress Series (***1998***), 1167(Progress in Forensic

Genetics 7), 249-251 CODEN: EXMDA4; ISSN: 0531-5131

Elsevier Science B.V.

AB FB Journal

English Collaborative research on the polymorphism of the STR locus HumFGA was collaborative research on the polymorphism of the STR locus HumFGA was carried out by the Institutes of Legal Medicine in 4 Italian regions: (Marches, Veneto, Lombardy, and Tuscany). The aim was to establish a database of allelic frequencies with a view to applying HumFGA in forensic identification and paternity testing. The goal for each participating identification and paternity testing. The goal for each participating lab. was to study .gtoreq.100 genotypes of unrelated, locally residing en i gardingi i jak

individuals. The results of statistical anal, were highly informative (PD = 0.78 and mean exclusion change = 0.71) suggesting that this system is a powerful tool for forensic routine.

CONT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

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1 R R C 5 ANSWER 3 OF 16 1996:681655 25:319487 CAPLUS CAPLUS COPYRIGHT 2004 ACS on STN

SO AU Structure of the human laminin .alpha.2-chain gene (LAVA2), which is affected in congenital muscular dystrophy Zhang, Xu; Vuolteenaho, Reetta; Tryggvason, Karl

Division Matrix Biology, Karolinska Institute, Stockholm, S-171 77, Swed. Journal of Biological Chemistry (***1996***), 271(44), 27664-27669 CODEN: JBCHA3; ISSN: 0021-9258

American Society for Biochemistry and Molecular Biology

8628

We have detd. the structure and complete exon size pattern of the human laminin .alpha.2-chain gene (LA-MA2), which has been shown to be affected in congenital muscular dystrophy (Helbling-Leclerc, A., Zhang, X., Topaloglu, H., Cruaud, C., Tesson, F., Weissenbach, J., Tome, F. M. S., Schwartz, K., Fardeau, M., Tryggvason, K., and Guicheney, P. (1995) Nat. Genet. 11,216-218). The gene is over 260,000 base pairs and contains 64 exons. The sequence of all exon-intron borders was detd. Two of the exons, i.e. exons 43 and 52, are extremely small in size, 6 and 12 base pairs, resp. Comparison of the exon pattern of the human LAMA2 gene with that of the Drosophila LAMA gene revealed that only 2 of 63 intron locations in the 5'-end of the human gene match the intron locations in the Drosophila gene, which contains 14 introns.

DN AN ANSWER 4 OF 16 CAPLUS COPYRIGHT 2004 ACS on CAPLUS SIN

124:48609

CS AU Fibrinogen .alpha. genes: conservation of bipartite transcripts and carboxy-terminal-extended .alpha. subunits in vertebrates Fu, Yiping, Cao, Yan; Hertzberg, Kathe M.; Grieninger, Gerd Lindsley F. Kimball Res. Inst. of the New York Blood Center, New York, NY,

10021, USA

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SO GENERAL CODEN: GNMCEP; ISSN: 0888-7543

8528 Academic

Journal

English
All three well-studied subunits of the clotting protein fibrinogen
(.alpha., .beta., .gamma.) share N-terminal structural homologies, but
until recently only the .beta. and .gamma. chains were recognized as
having similar globular C-termini. With the discovery of an extra exon in
the human fibrinogen .alpha. gene (exon VI), a minor form of the .alpha.
subunit (.alpha.E) with an extended .beta.— and .gamma.like C-terminus
has been identified (Fu et al., Biochem. 31, 1168, 1992). In the present
study, the polymerase chain reaction has been used to identify sequences
that encode counterparts to .alpha.E in chicken, rabbit, rat, and baboon.
The basic six-exon structure of the fibrinogen .alpha. genes is shown to be conserved among mammals and birds, as are the intron positions. Bipartite transcripts-still bearing an intron prior to the last exon-are found among the products of the various vertebrate fibrinogen .alpha.

> genes. The last exon represents the largest conserved segment of the gene and, in each species examd., encodes exactly 236 amino acids. The C-termini of these alpha. E chains align without a single gap and are between 76 and 99% identical. Since the exon VI-encoded domain of alpha. E is as well conserved as the corresponding regions of the .beta. and .gamma. chains, it follows that it is equally important and that alpha.E-fibrinogen plays a vital, if as-yet unrecognized physiol. role.

TI DA LS ANSWER 5 OF 16 CAPLUS COPYRIGHT 2004 ACS on 1995:667238 CAPLUS STN

123:49265

IN PA SO and merosin enhancement of neurite growth Nucleic acids encoding human merosin, merosin fragments and uses thereof

Engvall, Eva; Leivo, Ilmo La Jolla Cancer Research Foundation, USA

t. Appl., 65 pp. PIXXD2

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recombinant prodin of mercain, and the expression of recombinant proteins by use of a host vector system also are provided. The human mercain gene is mapped on human chromosome 6. The invention further provides the use of mercain to promote neurite growth and for certain diagnostic WO 1994-US10730 W 1994-US.

This invention provides an isolated nucleic acid mol. encoding a subunit of a protein, the protein having an apparent mol. wt. of about 800 kD, designated merosin. Also provided are isolated nucleic acid mols. which encode merosin fragments. Anti-merosin antibodies, vectors for the

ANSWER 6 OF 1995:393761 16 CAPLUS COPYRIGHT 2004 ACS on STN

CAPLUS

23:248220

ATRACES Cloning and expression of laminin .alpha.2 chain (M-chain) in the mouse Bernier, Suzanne M.; Utani, Atsushi, Sugiyama, Satoru; Doi, Toshio; Polistina, Claudio; Yamada, Yoshihko
Laboratory of Developmental Biology, National Institute of Dental
Research, Bethesda, MD, USA
Matrix Biology (***1995***), 14(6), 447-55

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CODEN: MTBOEC; ISSN: 0945-053X

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signal peptide. The amino acid sequence of the .alpha.2 chain shares a 45.9% identity with that of the .alpha.1 chain. Similar to the structure of the .alpha.1 chain, the .alpha.2 chain consists of several domains beginning at the N-terminus with three globular domains alternating with three epidermal growth factor-like domains followed by two .alpha.-helical domains and a C-terminal globular domain. The most N-terminal globular domain sand a C-terminal globular domain is highly conserved (77.3% identity) between the .alpha.2 and .alpha.1 chains, whereas the .alpha.-helical domains have low homol. (30.3% identity). Northern blot and RNase protection anal. revealed expression of mRNA for the .alpha.2 chain in heart, kidney, liver, skin, lung and skeletal muscle of newborn mice. Such a tissue distribution suggests a role for the .alpha.2 chain and, consequently, laminin-2 or -4 not only in the organization and the function of nerve and muscle tissue but possibly also in the mesenchymal components of certain tissues. full-length cDNA for the mouse laminin .alpha.2 chain. Four overlapping clones spanning 9,330 bp encode a predicted polypeptide of 3,106 amino acids having a calcd. mol. mass of 390 kDa including a 23-amino-acid membranes. Laminin-2, consisting of .alpha.2, .beta.1, and .gamma.1 chains, was originally identified in the basement membranes of skeletal muscle and peripheral nerve. The authors have isolated and sequenced the Inglish English English are a family of heterotrimeric glycoproteins specific to basement Laminins are a family of heterotrimeric glycoproteins specific to basement Laminins are a family of heterotrimeric glycoproteins.

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UF 06226388 A2
UF 06226388 A2
UF 0441141 B1
AI DE 1992-166930 A3
US 1996-72704 A3
A method is described for of fibrinogen to yield C-German DE 4242736 EP 605797 EP 605797 Synthetic peptides from fibrinogen and anti-peptide antibodies for use in immunoassay and treatment of fibrinolytic disorders Kraus, Michael; Stueber, Werner PATENT NO. ANSWER 7 OF 1994:506510 Patent CODEN: GWXXBX Ger. Offen., Behringwerke AG, 121:106510 AT, OF 16 CAP 510 CAPLUS BE, Ğ, go. CAPLUS COPYRIGHT 2004 ACS on STN Germany A1 A1 B1 T3 A1 A1 A1 A1 A1 A1 A1 A1 A2 A2 A3 DK, 19990317 , ES, FR, 19991109 20020827 19990616 19940630 19970327 DATE 19940618 19921217 19970204 19990415 19940713 19940623 19961008 19931215 GB, AT 1993-119574 ES 1993-119574 AU 1993-52435 S Q & SI SI DE 1992-4242736 EP 1993-119574 IT, APPLICATION NO. S 1993-166930 A 1993-2111645 P 1993-344306 S 1996-727045 1999-408172 LI, LU, NL, ŢŢ, SE 19931215 <--19931216 <--19931217 <--19961008 19921217 19931209 19931215 19931209 19990929 9931209 î î î

antigenic. The peptides are injected into rabbits to produce antibody-producing cells which are used to generate monoclonal antibodies for use in immunoassays or in the treatment of fibrinolytic disorders.

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ANSWER 8 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN

.994:126557 CAPLUS

.20:126557

12 Z Z 56 5 Human laminin M chain (merosin): complete primary structure, chromosomal assignment, and expression of the M and A chain in human fetal tissues Vuolteenaho, Reetta; Nissinen, Marja; Sainio, Kirsi; Byers, Mary; Eddy, Roger; Hirvonen, Harri; Shows, Thomas B.; Sariola, Hannu; Engvall, Eva; Tryggvason, Karl

Biocent., Univ. Oulu, Oulu, FIN-90570, Finland Journal of Cell Biology (***1994***), 124(3), 381-94 CODEN: JCLBA3; ISSN: 0021-9525

SO

English

853

that the M chain was expressed in most tissues such as cardiac muscle, pancreas, lung, spleen, kidney, adrenal gland, skin, testis, meninges, choroid plexus, and some other regions of the brain, but not in liver, thymus, and bone. In situ hybridization localized the expression of the M chain gene to cells of mesenchymal origin. In contrast, expression of the A chain was obed. only in kidney, testis, neuroretina and some region of brain as decid. by Northern analyses. Epithelial and endothelial cells were neg. for both M and A chain gene transcripts. The gene for the human M chain (LAPM) was localized to chromosome 6q22.fwdarw.23. clones isolated from human placental libraries. The clones covered a total of 6942 bp, with 49-bp encoding a 5' end untranslated region and 6893-bp coding for a translated sequence. The complete human laminin M chain contains a 22-residue signal peptide and 3,088 residues of the mature M chain. The M chain has a domain structure similar to that of the human and mouse A chains. The homol, between the two human laminin heavy chains is highest in the short arm region and lowest in the long arm chains is highest in the short arm region and lowest in the long arm chains is highest in the long arm the local domain I + II. Northern blot anal, of human fetal tissues showed helical domain I + II. The primary structure of the human laminin M chain was detd. from

ANSWER 9 OF 16 CAPLUS 1993:489199 CAPLUS COPYRIGHT 2004 ACS on STN

DN AN 19:89199

Carboxy-terminal-extended variant of the human fibrinogen .alpha. subunit:

a novel exon conferring marked homology to .beta. and .gamma. subunits Fu, Yiping; Weissbach, Lawrence; Plant, Patricia W.; Oddoux, Carole; Cao, Yan; Liang, T. Jake; Roy, Samar N.; Redman, Colvin M.; Grieninger, Gerd Lindsley F. Kimball Res. Inst., New York Blood Cent., New York, NY, 10021,

Biochemistry (***1992*** BICHÁW; ISSN: 0006-2960

Journal CODEN:

SO S ΑU

USA

& F. F.

Similarities between the N-terminal regions of the three subunits of the clotting protein fibrinogen-(.alpha., beta., .gamma.)2-suggest that they evolved from a common progenitor. However, to date no human .alpha. chain has been found with the strong C-terminal homol. shared by the .beta. and .gamma. chains. The natural product of a novel fibrinogen .alpha. chain transcript bearing a sep. open reading frame that supplies the missing C-terminal homol. to the other chains is examd. Addhl. splicing leads to the use of this extra sequence as a sixth exon elongating the .alpha.

B

for obtaining synthetic peptides by plasmin cleavage iC-terminal ends of the E fragment which are also

chain by 35%. Since the extended .alpha. chain (.alpha.E) is assembled into fibrinogen mois. and its synthesis is enhanced by interleukin-6, it suggests participation in both the acute phase response and normal

ANSWER 10 OF 1992:544541 CAPLUS 117:144541 CAPLUS COPYRIGHT 2004 ACS 9

TI DN AU CS SO Nucleotide sequences of the three genes coding for human fibrinogen Chung, Dominic W.; Harris, Jeff E.; Davie, Earl W.
Dep. Biochem., Univ. Washington, Seattle, WA, 98195, USA
Advances in Experimental Medicine and Biology (***1990***),
281 [Fibrinogen, Thromb., Coagulation, Fibrinolysis), 39-48
CODEN: AEMBAP; ISSN: 0065-2598

English Journal; General Review

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The gene for the A.alpha. chain of human fibrinogen was isolated by plaque hybridization of recombinant lambda phage genomic libraries using cDNAs as hybridization probes. The A.alpha. gene is located at the 3' end of the gamma. gene and consists of 5 exons. Three single nucleotide differences with the cDNA sequence were obsd., but they do not change the amino acids encoded. The majority of the primary translation product (amino acids 13-625) is encoded in one large exon which also contains the tandem repeats unique to the A.alpha. chain. Another unique feature of this gene is that it contains a segment of 100 residues in intron C that are exclusively pyrimidines and >70% T residues. The sequences of the B.beta.

12 N 25 6 ANSWER 11 OF 16 CAPLUS 03:173275 1985:573275 CAPLUS COPYRIGHT 2004 ACS 9 SIN

Evolution and structure of the fibrinogen genes.

Random insertion of

SO ΑU Albert J., Jr.; Malley, James D.; Kant, Jeffrey A. Med. Sch., Stanford Univ., Stanford, CA, 94305, USA Journal of Molecular Biology (***1985***), 185(1), 1-19 CODEN: JMOBAK; ISSN: 0022-2836 introns or selective loss?
Crabtree, Gerald R.; Comeau, Claudette M.; Fowlkes, Dana M.; Fornace,

AB LA DI

Yet, when the 3 fibrinogen chains are aligned by amino acid homol, the positions of intervening coincide at only 2 positions for all 3 chains. Whereas I addnl. intron occurs at a homologous site in the .beta. and .gamma. chains, none of the positions of the remaining I1 introns in the 3 genes is shared. This arrangement of introns in the 3 fibrinogen genes suggests that either introns were selectively lost, implying that there is essential information in the retained introns, or the common introns were present in the ancestral fibrinogen gene and introns have been randomly inserted since the triplication of the original gene. The more likely possibility of selective loss of introns implies that the ancestral gene, as it existed, apprx.1 billion years ago, must have been composed of Chromosomal linkage as well as sequence homologies provide unequivocal evidence that the genes for the .alpha., .beta. and .gamma. chains of fibrinogen arose by successive duplication of a single ancestral gene.

> ANSWER 12 OF 1983:517030 CAPLUS CAPLUS COPYRIGHT 2004 ACS

SO Partial mRNA sequences for human A.alpha., B.beta., and .gamma. fibrinog chains: Evolutionary and functional implications Kant, Jeffrey A.; Lord, Susan T.; Crabtree, Gerald R. Lab. Pathol., Natl. Cancer Inst., Bethesda, MD, 20205, USA Proceedings of the National Academy of Sciences of the United States of America (***1983***), 80(13), 3953-7 fibrinogen

CODEN: PNASA6; ISSN: 0027-8424

£ 5

Rat cDNA and genomic probes were used to screen a human liver cDNA library to isolate clones of 2274, 855, and 736 base pairs (bp) coding for the A.alpha. B.beta., and .gamma. chains of human fibrinogen. Sequence anal. reveals a hitherto unrecognized extension of 15 amino acids at the C-terminus of the A.alpha. chain, the terminal residue of which is proline. This brings the known length of the human A.alpha. chain to 625 amino acids. The 13-amino acid repeated region in the midportion of the A.alpha. chain clearly has arisen through an 8-fold duplication of a 39-bp genetic element, which itself appears to have been constructed from smaller 6-bp repeating units. Greater than 508 sequence homol. between B.beta. and .gamma. chain coding regions confirms that these genes have arisen by duplication and subsequent divergence of an ancestral gene. A comparison of human and subsequent divergence of an ancestral gene. A comparison of human and rat .gamma. chain cDNAs shows >888 sequence homolover the C-terminal 162 amino acids, implying strong selective pressures on these portions of the :gamma. chain gene.

ANSWER 13 OF 1983:417447 16 CAPLUS COPYRIGHT 2004 ACS on STN CAPLUS

TI DN TI

Characterization of a complementary deoxyribonucleic acid coding alpha. chain of human fibrinogen Rixon, Mark W.; Chan, Wai Yee; Davie, Earl W.; Chung, Dominic W. Dep. Blochem., Univ. Washington, Seattle, WA, 98195, USA Biochemistry (***1983***), 22(13), 3237-44 CODEN: BICHAW; ISSN: 0006-2960

B F F SO Journa.

A human liver cDNA library was screened for the alpha. chain of fibrinogen with a cDNA clone from the corresponding bowine mol. as a hybridization probe. Several human clones coding for the alpha. chaiwere identified, and 1 of these was used to rescreen the entire cDNA library of 18,000 recombinants. Plasmids with the largest cDNAs were

isolated, and their inserts were sequenced. The largest cDNA insert contained 2224 base pairs, including a noncoding region at the 5' end that was followed by a region coding for a signal peptide of 19 (or 16) amino acids and a mature protein of 625 amino acids, a stop codon of TAG, another noncoding region, and a poly(A) tail at the 3' end. Eight tandem repeats of 39 base pairs were obsd. which started with nucleotide 905 (amino acid residue 270) and ended with nucleotide 1213 (amino acid residue 372). The identity in the nucleotide sequence in the tandem repeats ranged 72-95% when compared to a consensus sequence. The predicted amino acid sequence for the mature polypeptide chain was 15 amino acids longer at the C-terminal end than that of the .alpha. chain isolated from plasma fibrinogen and sequenced. Apparently, minor proteolysis of the C-terminus of the .alpha. chains had occurred, probably

during secretion or circulation of the protein in plasma

Max-Planck-Inst. Blochem., Martinssied, D-8033, Fed. Rep. Ger. Protides of the Biological Fluids (***1980***), 28th, 51-6 CODEN: PBFPA6; ISSN: 0079-7065 .gamma.-chain with considerably lower mol. wt. seem to be present in all individuals. The structural error in a new abnormal variant, fibrinogen Muenchen, has recently been identified as an Arg .fwdarw. Asn exchange in position 3 of the .alpha.-chain. Human fibrinogen has the overall structure (A.alpha., B.beta., gamma.)2. The complete amino acid sequences of the 3 chains with 610, 461, and 411 residues have been elucidated. The chains are hald together by 29 SS bonds, 3 of which link the half-mols. to each other. Carbohydrate side structural variants
Henschen, A.; Lottspeich, F.; Southan, chains are present in the B.beta.- and .gamma.-chains. English NSWER 14 OF 1981:116302 CAPLUS CAPLUS sequence, sulfur bridges, COPYRIGHT 2004 ACS 9 glycosylation and some Variants of the

ATRACES ANSWER 15 .980:17417 OF 16 F 16 CAPLUS CAPLUS COPYRIGHT 2004 ACS 8 STN

SO SO Dep. Chem., Univ. California, San Diego, CA, 92093, USA Nature (London, United Kingdom) (***1979***), 280(5722), 464-8 CODEN: NATUAS; ISSN: 0028-0836 The amino acid sequence of the .alpha.-chain of human fibrinogen Doolittle, R. F.; Watt, K. W. K.; Cottrell, B. A.; Strong, D. D. D.; Riley,

The structure of human fibrinogen .alpha.-chain could be divided into zones of .appxx.200 residues, each of unique amino acid compn. The regions were designated ZN, ZM, and ZC and corresponded roughly to the amino-terminal third, the middle third, and the carboxy-terminal third resp. ZM contained the 2 primary .alpha.-chain crosslinking acceptor sites and consisted of a series of internal duplications. English third, the

ANSWER 16 OF 16 | 1980:1856 CAPLUS CAPLUS COPYRIGHT 2004 ACS 9 SIN

Amino acid sequence studies on the .alpha. chain of human fibring overlapping sequences providing the complete sequence Watt, K. W. K.; Cottrell, B. A.; Strong, D. D.; Doolittle, R. F. Dep. Chem., Univ. California, La Jolla, CA, 92093, USA Biochemistry (***1979***), 18(24), 5410-16 of human fibrinogen.

CODEN: BICHAW; ISSN: 0006-2960

AB DI

The complete amino acid sequence of the alpha. chain of human fibrinogen was detd. It contains 610 amino acid residues and has a calcd. mol. wt. of 66,125. The chain has 10 methionines, and fragmentation with QNBr yielded 11 peptides. The arrangement of the 11 fragments was detd. by this isolation of peptide overlaps from plasmic and staphylococcal protease by the

digests of fibrinogen and(or) .alpha. chains. In addn., certain of the CNBr fragments, preliminary reports of whose sequences have appeared previously, were resexand. to resolve several discrepancies. The .alpha. chain is homologous with the .beta. and .gamma. chains of fibrinogen, although a large repetitive segment of unusual compn. is absent from the latter 2 chains. The existence of this unusual segment divides the sequence of the .alpha. chain into 3 zones of .apprx.200 residues each that are readily distinguishable on the basis of amino acid compn. alone

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The present invention provides peptides, peptide dimers, and multimeric complexes comprising at least one binding moiety for KDR receptor or vascular endothelial growth factor (VEGF)/KDR complex, which have a
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PCT. Int. Appl., 470 pp.
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variety of uses wherever treating, detecting, isolating, or localizing angiogenesis is advantageous. Particularly disclosed are synthetic, isolated peptides capable of binding KDR or VEFG/KDR complex with high affinity (e.g., having a KD < 1 .mu,M), and dimer and multimeric constructs comprising these polypeptides. The involvement of VEGF and KDR in angiogenesis makes the binding peptides particularly useful for imaging important sites of angiogenesis, e.g., neoplastic tumors, for targeting substances, e.g., therapeutics, including radiotherapeutics, to such sites, and for treating certain disease states, including those assocd. with inappropriate angiogenesis.

RE.GNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

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Sato, Aaron K.; Sexton, Daniel J.; Dransfield, Daniel T.; Ladner, Robert

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PROTEIN SEQUENCE; STEREOSEARCH

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type	loc	tic	description
terminal mod.	Trp-1	'	N-acetyl
terminal mod.	Lys-19	1	C-terminal amide
bridge	Cys-4	- Cys-12	disulfide bridge
modification	Lys-19	1	undetermined modification

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

Not Given|W02003074005

SEQID 336

SEQ3 1 Trp-Gln-Pro-Cys-Pro-Trp-Glu-Ser-Trp-Thr-

11 Phe-Cys-Trp-Asp-Pro-Gly-Gly-Gly-Lys

HITS AT: 1-15

RELATED SEQUENCES AVAILABLE WITH SEQLINK

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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Binding peptides for the KDR receptor and vascular endothelial growth factor/KDR complex and their use in diagnosis, therapy, and imaging of angiogenesis-related disorders 141:167846 CA

C.; Arbogast, Christophe; Bussat, Philippe; Fan, Hot Linder; Karen E.; Marinelli, Edmund R.; Manjappan, ii Adrian; Pillai, Radhakrishna; Pochon, Sibylle; Ramal Shrivastava, Ajay; Song, Bo; Svenson, Rolf E.; Von W 20 Dyask Corp., USA; Bracco International B.V. PA Dyask Corp., USA; Bracco International B.V. PATENT NO. PATENT NO. PATENT NO. W. 204065621 Al 2040805 W0 2003-US2878	THIS	~	FOR	AVAILABLE F	VAII	:	RENC	REFERENCES	Ü		E ARE 4 C	THERE	THE		RE. ONT
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51 Lys-Gly-Thr-Gly-Leu-Arg-Gly-Gln-Glu-Leu-
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Ruben, Steven M.; Barash, Steve C.; Birse, Charles E.; Rosen, Craig A.

Human Genome Sciences, Inc., USA

U.S. Pat. Appl. Publ., 174 pp., Cont.-in-part of Appl. No. PCT/US00/26524. US 2003109690 WO 2001022920 English CODEN: USXXCO Patent : AE, AG, CR, CU, HU, ID, LU, LV, SD, SE, YU, ZA, A1 20030612
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Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K.
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Fibrin binding moieties useful as imaging agents
Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K.
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1 Cys-Tyr-Phe-Cys-Pro-Gly-Glu-Pro-Trp-Thr
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11 Phe-Cys-Cys-Asp-Asp

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11 Leu-Cys-Leu-Gly-Val

1 Trp-Leu-Asn-Cys-Gly-Trp-Gly-Ser-Gly-Lys-

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Fibrin binding moleties useful as imaging agents
Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. PATENT NO. 137:90279 CA KIND DATE
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Fibrin binding moieties useful as imaging agents
Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. U.S. Pat. Appl. Publ., 41 pp. CODEN: USXXCO PATENT NO. Patent Patent KIND DATE A1 20030731 20011221 KIND DATE 20020718 20030327 FR, GB, GR, IT, LI, LU, MK, CY, AL, TR
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Fibrin binding moieties useful as imaging agents
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Fibrin binding moieties useful as imaging agents
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Dyax Corp., USA
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Fibrin binding moieties useful as imaging agents
Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K.
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Wescott, Charles R.; Beltzer, James P.; Sato, Aaron K. 139:138721 CA
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Wescott, Charles R.; Baltzer, James P.; Sato, Aaron K. PATENT NO. MIND DATE
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substance identification. This file contains CAS Registry Numbers for easy and accurate

=> s 145 and py<=2001 21560072 PY<=2001 L62 3057 L45 AND PY<=2001

=> s 162 52224 FIBRIN? and fibrin?

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ANSWER 1 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN 2004:749051 CAPLUS

SO SO ΞZ Munin Corporation, USA
U.S., 61 pp., Cont.-in-part of U.S. Ser. No. 142,569. Cysteine-rich extracellular matrix signaling molecules, protein and sequences thereof, and drug screening methods using the same CODEN: USXXAM Lester F.

ΡĮ LA English FAN. CNT 3 US 6790606
W0 973395
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W: AL, AM, LE, FI, LT, LU, LT, LU, SE, SG, SG, SH, KE, GR, KE, GR, LE, PATENT NO. Patent A2 A3 A3 A0 A3 A0 A3 A3 A3 A3 KIND AZ, BB, BG,
HU, IL,
KG, MK, MY,
SK, TJ, TM,
RU, TJ, TM,
SD, SZ, UM,
SD, SZ, UM 20040914 19970918 19980108 DATE JP, SE, US 1999-142569 WO 2001-US3267 计交叉员 US 2000-495448 WO 1997-US4193 APPLICATION NO. ᄩ 5888 5 면 된 된 CH, CN, KP, KR, NZ, PL, UG, US, G, E (G 및 UZ, CI, 3,5 ₹8££ 20000131 19970314 19990402 20010131 DATE FR, DK, EE, LR, LS, RU, SD, AM, AZ, 98

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Protain and cDNA sequences for mammalian extracellular matrix (ECM) protain and cDNA sequences for mammalian extracellular matrix (ECM) signaling mols. affecting the cell adhesion, migration, and proliferation activities, namely Cyr61, Fispl2, CTGF, are provided. The polypeptide compns. comprise mammalian ECM signaling mols. peptide fragments, inhibitory peptides capable of interacting with receptors for ECM signaling mols., and antibody products recognizing Cyr61. Also provided are methods for producing mammalian ECM signaling mols. Further provided are methods for producing mammalian ECM signaling mols. For screening modulators of cell migration as well as methods to modulate angiogenesis, and oncogenesis. Claimed is a method for screening computation of cell migration and human computation.
             modulators of cell migration using gel matrix comprising Cyr61 and human fibroblast cells presenting .alpha.6.beta.1 integrin.
VI 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
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Lewis, Claire; Staton, Carolyn University of Shaffield, UK PCT Int. Appl., 41 pp. CODEN: PIXXD2

use in cancer therapy

Anti-angiogenic polypeptides derived from

fibrinogen E and their

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Patent

WO 2001088129 PATENT NO.

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D.; Hsieh,

Chung-Ming;

Yet, Shaw-Fang; Perrella, Mark A.; Lee,

Layne, Matthew

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WO 2001-GB2079 APPLICATION NO.

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11 P A L 66 DN DN AB CIB SO S ď RE. Æ PRAI plasmid-assocd. DNA exchange between Y. pestis and the exclusively human pathogen Salmonella enterica serovar Typhi.

ONT 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD Q Q BR 2001010800 A 2003031 BR 2001-10800 20010514
JP 2003533204 T2 20031111 JP 2001-584511 20010514
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GB 2000-1370 A 20001109
WD 2001-GB2079 W 2001109
WD 2001-GB2079 W 2001109
The invention relates to the anti-angiogenic effects of polypeptides derived from ***fibrinogen*** Specifically, ***fibrinogen*** E peptides of amino acid 1-78 of .alpha. chain, 43-122 of .beta. chain, and 1-62 of .gamma. chain are identified an chain, 43-122 of .beta. chain, and 1-62 of .gamma. chain are identified an chain, 43-122 of .beta. chain, and 1-62 of .gamma. chain are identified an chain, 43-122 of .beta. Chain, and 1-62 of .gamma. chain are identified and chain are definited and chain are identified and chain are larger than a chain are identified and chain are larger than a chain a chain are larger than a chain a chain are larger than a chain a c Yersinia pestis pFra shows biovar-specific differences and recent common ancestry with a Salmonella enterica serovar typhi plasmid Prentice, Michael B.; James, Keith D.; Parkhill, Julian; Baker, Stephen G.; Stevens, Kim; Simmonds, Mark N.; Mungall, Karen L.; Churcher, Carol; Oyston, Petta C. F.; Titball, Richard W.; Wren, Brendan W.; Wain, John; Pickard, Derek; Hien, Tran Tinh; Farrar, Jeremy J.; Dougan, Gordon Department of Medical Microbiology, St. Bartholomew's and the Royal London School of Medicine and Dentistry, London, ECIA 78E, UK Journal of Bacteriology (***2001***), 183(8), 2586-2594 CODEN: JOBAAY; ISSN: 0021-9193 American Society for Microbiology CHIF, a novel cycle-like factor, regulates the circadian oscillation of plasminogen activator inhibitor-1 gene expression
Maemura, Koji; De la Monte, Suzanne M.; Chin, Michael T.; Layne, Matthe systemic pathogen. However, the origin of Y. pestis-specific plasmids remains obscure. The authors demonstrate specific plasmid rearrangements in different Y. pestis strains which distinguish Y. pestis by. Orientalis strains from other biovars. The authors also present evidence for Population genetic studies suggest that Yersinia pestis, the cause of plague, is a clomal pathogen that has recently emerged from Yersinia pseudotuberculosis. Plasmid acquisition is likely to have been a key element in this evolutionary leap from an enteric to a flea-transmitted systemic pathogen. However, the origin of Y. pestis-specific plasmids ANSWER 3 OF 14 CAPIUS COPYRIGHT 2004 ACS on STN 2001:262857 CAPIUS E 2000:871614 134:145618 ANSWER 4 OF 14 CAPLUS 135:340130 Journal VZ, RW: GH, DE, BJ, P 1285063 ALL CITATIONS AVAILABLE IN THE RE FORMAT ALL CITATIONS AVAILABLE IN THE RE FORMAT , BE, 경험관 CAPLUS Ę, GES, DK, ES, FR, FI, RO, MK, QR, ZW, COPYRIGHT 2004 ACS on STN & & & & 2 F S & Ĭ, TAT, TM BE, CH, SE, TR, TG SE, MC, 20010514 E, MC, PT,

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- SO Journal of Biological Chemistry (***2000***), 275(47), 36847-36851 Cardiovascular Division, Brigham and Women's Hospital, Harvard Medical School, Boston, MA, 02115,
- American Society for Biochemistry and Molecular Biology

AB PH

circadian oscillation of PAI-1 gene expression in endothelial cells. In addn. the results potentially provide a mol. basis for the morning onset CIOCK and up-regulates the PAI-1 gene through E-box sites. Furthermore, Period2 and Cryptochrome!, whose expression show a circadian oscillation in peripheral tissues; inhibit the PAI-1 promoter activation by the CIOCK:CLIF heterodimer. These results suggest that CLIF regulates the helix-loop-helix (bHLH)/PAS domain transcription factors play a crucial role in controlling the biol. clock that controls circadian rhythm. The authors isolated a novel bHLH/PAS protein, cycle-like factor (CLIF) from human umbilical vein endothelial cells. CLIF shares high homol. with Drosophila CYCLE, one of the essential transcriptional regulators of circadian rhythm. CLIF is expressed in endothelial cells and neurons in of myocardial infarction. circadian rhythm. CLIF is expressed in endothelial cells and neurons in the brain, including the suprachiasmatic nucleus, the center of the circadian clock. In endothelial cells, CLIF forms a heterodimer with oscillation and may account for the morning onset of myocardial infarction. However, the mol. mechanisms regulating this circadian oscillation remain unknown. activity. it may partly result from circadian variation of ***fibrinolytic**
ivity. Plasminogen activator inhibitor-1 activity shows a circadian onset of myocardial infarction occurs frequently in the early morning it may partly result from circadian variation of ***fibrinolytic*** Recent evidence indicates that basic

RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

T D A L PRAI PI SO SD SD SD and their use in diagnosis and therapy Grieninger, Gerd; Applegate, Dianne; S The New York Blood Center, Inc., USA PCT Int. Appl., 66 pp. US 6416963 EP 1105428 WO 2000009562 PATENT NO. English 2000:133731 132:177254 ANSWER 5 OF 14 Patent CODEN: PIXXD2 ***Fibrinogen*** 1998-96210P 1999-373157 1999-US18412 W: CA, JP
RW: AT, BE,
PT, SE 2002168722 AT, BE, IE, FI CAPLUS COPYRIGHT 2004 ACS on STN 요 유 KIND fragments, their production with recombinant cells, Al Ž DE, DK, 20020709 20021114 19980812 DATE 19990812 19990812 20010613 20000224 ES, FR, DK, ES, GB, FI, Stoike-Steben, Lara US 1999-373157 US 2002-112527 EP 1999-941108 WO 1999-US18412 APPLICATION NO. GR, FR, GB, IT, LI, LU, GR, IE, Ä, IT, SE, MC, PT, LU, MC, NL, 19990812 19990812 <--Ŷ

> behavior -340 in clot formation and proteolytic susceptibility. Plasmin rapidly released the alpha EC domain of ***fibrinogen** -420 and this fragment was resistant to further degradn in vitro. This alpha EC fragment is detectable in the plasma of patients undergoing thrombolytic Methods of treating disease characterized by ***fibrinogen*** metab are also disclosed. In addn., the invention also provides monospecific antibodies which are specifically reactive with .alpha.EC domain of ***fibrinogen*** and methods for detecting and purifying these
> fragments. The method of the invention also includes a diagnostic method
> for detg. ***fibrinolytic*** states or atherogenesis in a mammal. The invention provides novel .alpha.ECX cleavage fragments of ***fibrinogen*** and methods for detecting and purifying therapy. .alpha.ECX cleavage fragments of ***fibrinogen*** ***fibrinogen*** Also provided, are DNA and RNA mols. that encode agments of ***fibrinogen*** In addn., the -420 was similar to that of states or atherogenesis in a mammal racterized by ***fibrinogen*** met ***fibrinogen*** metab.

ANSWER 6 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN 1999:621254 CAPLUS

THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

AN DN 132:118097

CS DNA sequence of the canine platelet .beta.3 gene from cDNA: comparison canine and mouse .beta.3 to segments that encode alloantigenic sites are functional domains of .beta.3 in human beings npartson of sites and

SO Lipscomb, Desiree L.; Bourne, Candace; Boudreaux, Mary K. Department of Pathobiology, College of Veterinary Medicin University, Auburn, AL, 36649, USA Journal of Laboratory and Clinical Medicine (***1999***), 134(3), College of Veterinary Medicine, Auburn

JLCMAK; ISSN: 0022-2143

Mosby, Inc.

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platelet """ Fibringen"" binding and platelet aggregation. This study was designed to characterize the nucleotide sequence of the canine platelet beta.3 gene from cDNA. The nucleotide and deduced amino acid sequences of the canine beta.3 gene were 92% and 96% homologous, resp., with the sequences previously established for the beta.3 gene of human beings. Within the beta.3 gene, the nucleotide sequence of cDNA prepd from canine platelets shared homol. of 89% for the cytoplasmic domain, 93% for the transmembrane domain, 92% for the extracellular domain, 94% for the arginine-glycine-aspartic acid (RG) binding domain, and 97% for the region assocd with Ga2+dependent stabilization of the alpha. Ib. beta.3 """ binding pocket. The deduced amino acid sequence of the contraction of the of the cont The platelet glycoprotein complex .alpha.IIb.beta.3 is required for platelet - ***fibrinogen*** binding and platelet aggregation. The

of .beta.3 in human beings. The canine platelet cDNA signal peptide segment of the .beta.3 gene encodes for 22 amino acids, as compared with 26 amino acids previously reported for human beings. The deduced amino acid sequence of canine .beta.3 corresponds to the high-frequency allelic ***fibrinogen*** -binding pocket. The deduced amino acid sequence of canine beca. 3 was 100%, 97%, 96%, and 95% homologous with the cytoplasmic, transmembrane, extracellular, and RGD-binding domains, resp., and was 100% homologous with the region assocd. with Ca2+-dependent stabilization of the .alpha.IIb.beta.3 ***fibrinogen*** -binding pocket

form for five of the six alloantigenic sites reportedly assocd, with human platelets: Leu3Jleu40Pro407Arg489Arg636. The apparent amino acid residue in position 143 (Pen alloantigen) of canine platelet beta.3 is histidine compared with arginine in human beings. Knowledge of the beta.3 gene nucleotide sequence of normal dogs will facilitate the understanding of platelet alpha.1ID.beta.3 structure-function relationships.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human Ig heavy chain sequence capable of differentiating between the HPA-1a protein and the HPA-1b protein was isolated from the repertore of an alloimmunized individual. This antibody fragment detected HPA-1a in
Smithkline Beecham Corporation, USA; Black, Michael Terence; Hodgson, John Edward; Knowles, David Justin Charles; Lonetto, Michael Arthur; Nicholas, Richard Oakley; Stodola, Robert King PCT Int. Appl., 640 pp.
                                                                                                                           predicted protein products, and their diagnostic and therapeutic uses Black, Michael Terence; Hodgson, John Edward; Knowles, David Justin Charles; Lonetto, Michael Arthur; Nicholas, Richard Oakley; Stodola,
                                                                                                                                                                                                                                                                                                                                                                                                     flow cytometry and inhibited ***fibrinogen*** binding and plately aggregation. The antibody may have potential for understanding key aspects of the HPA-1 antigen-antibody interaction and for developing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification of human heavy chain antibody fragment directed against human platelet alloantigen la (HPA-la)
Kickler, Thomas S.; Kennedy, Sean D.; Okamoto, Naoaki
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                                                                                                      Robert King
                                                                                                                                                                                                         Genomic DNA sequences of Streptococcus pneumoniae strain 0100993, their
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	se of su	iosynthesis or	of antimicrobial drugs. This invention also	encoded protein in	φ	provided that are	Thus, 322 DNA fragment sequences and 392	recombinant host c	well as the prodn.	polynucleotides, t	Newly identified p	US 1997-978454	US 1997-977555	US 1997-958668	_		ш		S	US 2002091236	US 6348578	US 6171835	US 6284878	US 5932701	US 6165762	US 6310193	80		EP 956289	RW: AT, BE, CH,	W: JP, US	WO 9806734	PATENT NO.	English .QNT 13	Patent	CODEN: PIXXD2
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TLABLE IN	in therapy.	such poly	his inven	re initia	each DNA	d by Stre	mences an	nsformed	1 polymucl	of such p	otides, p	19971125	19971125	19971027	19970815	19970815	19970708	19970210	19960816	20020711	20020219	20010109	20010904	19990803	20001226	20011030	20001031	, GB, IT,		C, ES, FI,		19980219	DATE			
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	8 F CO 8 D	and	μ.	for the screening	open reading	strain 0100993	sequences are	es, are provided.	es and	ypeptides, as	by such								,	20010518	19991014	19990830 <	19971215 <	19971125 <	19971027 <	19970930 <	19970815 <		19970815 <	LU, MC, NL, PT, SE		80	DATE	6		

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TI AN ANSWER 9 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN 1997:498657 CAPLUS 1297:187186 Expression of two novel recombinant proteins from aortic adventitia (Kappafibs) sharing amino acid sequences with cytomegalovirus ozsywath, Kathleen J., Hirose, Hitoshi, Xia, Shichao; Chew, David; Knoetgen, James, III; Tilson, M. David

Columbia University and Department of Surgery of the St. Luke's-Roosevelt Hospital Center, New York, NY, 18019, USA Journal of Surgical Research (***1997***), 69(2), 277-282 CODEN: JSGRA2; ISSN: 0022-4804

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We have recently purified and partially sequenced a microfibrillar protein

Pos. plaques were purified and expressed in a strain of Escherichia coli. The clone sequences were analyzed. The expressed proteins were sepd. by SDS/PAGE and the immunoblots were probed with either AAA IGG or anti-human Ig .kappa. antibody. Exptl. cell lines, transfected with the clones (clones 1 and 5), synthesized recombinant proteins (rAAAP-CLI) and rAAAP-CLI) detectable in Western immunoblots with AAA IGG. A prediction of the tertiary structure resembles well-characterized cell adhesion mols. These findings suggest that there is a novel family of matrix proteins that there is a novel family of matrix proteins. from human acrtic adventitia (aneurysm-assocd antigenic protein, 40 kDa (AAAP-40)) that is immunoreactive with 1g (1gG) from the wall of abdominal acrtic aneurysms (AAAs). It shares notifs with 1g .kappa. (which may act as a binding site for interaction with integrins), cytomegalovirus (which may be a mol. mimic in the pathogenesis of AAA), and vitronectin and the ***fibrinogens*** A cDNA library was constructed from the acrtic adventitia of a AAA. The library was screened with either rabbit anti-vitronectin antibody or rabbit anti- ***fibrinogen*** antibody. that may use Ig motifs as binding sites for cellular integrins and that there are matrix proteins in addn. to AAAP-40 that may serve as autoantigens in the pathogenesis of AAA disease.

ANSWER 10 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN 1993:554328 CAPLUS 119:154328

A comparative analysis of cDNA-derived sequences for rat and mouse .beta.3 integrins (GPIIIA) with their human counterpart Cieutat, A. M.; Rosa, J. P.; Letourneur, F.; Poncz, M.; Rifat, S. Hop. Lariboisiere, Paris, Fr. Biochemical and Biophysical Research Communications (***1993***),

SO

CODEN: BBRCA9; ISSN: 0006-291X

English

853

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fibrinogen , is a member of the integrin superfamily. Cloning of the mouse and rat .beta.3 cDNAs is described here. These data represent the first available non-human .beta.3 sequences, allowing important comparative analyses. Both .beta.3 sequences are highly homologous with human .beta.3, well above the av. rodent-human protein homol. of 79%. The ligand binding domains (amino acids 109-171 and 204-229) are, resp., 90% and 100% homologous. The .beta.3 transmembrane and the cytoplasmic tail are surprisingly highly conserved, being 97% and 100% homologous, resp., but share little homol. with .beta.1, or .beta.2. This latter difference argues strongly in favor of a crucial .beta.3-specific function for these domains. In conclusion the first comparative anal. of .beta.3 chains demonstrates a high overall homol. The biol. implications of these comparisons are discussed.

SO PA DI A A 66 ANSWER 11 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN 991:37194

114:37194

Recombinant manufacture of soluble functional integrins Bodary, Sarah C.; Gorman, Cornelia M.; McLean, John W.; Napier, Mary A. Genentech, Inc., USA

PCT Int. Appl., 47 pp. CODEN: PIXXD2

Patent

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make them therapeutically useful and as reagents for the deth. of their ligands. A cDNA for GPIIb was cloned using an oligonucleotide probe and a cDNA for GPIIA of the prior art obtained and modified to lower the G/C content of the 5' region. Expression vectors for the two cDNAs were introduced into 293S cells and transformants shown to produce the membrane-bound complex. The cDNAs were then modified to introduce stop codons into the sequence immediately before the coding sequences for the transmembrane domains. 293S cells transformed with the appropriate plasmids were shown to produce the sol. diner. Clones stably expressing the genes were established. The protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted as a dimer and was able to the definition of the protein was secreted. Human polypeptide receptors such as platelet glycoprotein GPIIb-GPIIIa are manufo. as a functional, i.e. ligand-binding, sol. dimer by expression of cDNAs for analogs lacking the transmembrane and cytoplasmic domains of the polypeptides. These sol. derivs. have altered physiol. properties that able to bind fibronectin.

ANSWER 12 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

1990:212623 CAPLUS

1 B & L 66 112:212623

Two contrary functions of tenascin: dissection of the active sites by

S & recombinant tenascin fragments
Spring, Juerg; Beck, Konrad; Chiquet-Ehrismann, Ruth
Friedrich Miescher-Inst., Basel, CH-4002, Switz.

AB LA SO Cell (Cambridge, MA, CODEN: CELLIB5; ISSN: Journal United States) (***1989***), 59(2), 325-34 0092-8674

6 arms of tenascin. In contrast, constructs contg. the 13 1/2 EGF-like repeats of tenascin showed an antiadhesive effect. The coexistence of the 2 contrary signals on the same mol. might be responsible for the versatile A structural and functional model of tenascin was elaborated using recombinant parts of 3 alternatively splitced tenascin variants and anti-tenascin monoclonal antibodies. The fusion proteins were compared with intact tenascin for their functions and by electron microscopy. A fragment also contains the epitope of the monoclonal antibody anti-Tn68, which inhibits cell attachment to tenascin and binds near the tips of the strong cell-binding site was localized within 104 amino acids. features of tenascin.

ANSWER 13 OF 14 CAPLUS COPYRIGHT 2004 ACS 1989:129541 CAPLUS 9

110:129541

TP A 6 Cloning of glycoprotein IIIa cDNA from human erythroleukemia cells and localization of the gene to chromosome 17

SO ΑU Rosa, Jean Philippe; Bray, Paul F.; Gayet, Odile; Johnston, Geoffrey I.; Cook, Richard G.; Jackson, Kenneth W.; Shuman, Marc A.; McEver, Rodger P.

Lariboisiere, Paris, d (***1988***), 7;

Blood (***1988***), 72(2), 593-600 CODEN: BLOOAW; ISSN: 0006-4971

a f g Journa.

was screened with a 30mer oligonucleotide derived from a platelet GPIIIa peptide, and three overlapping cNNAs were isolated. The three inserts encompassed 3.5 kilobases (kb), including the entire coding region of mature GPIIIa (2286 basepairs, bp) and 1.3 kb of 3' untranslated sequence. All 222 residues detd. directly from platelet GPIIIa tryptic peptides exactly matched the HEL cell-deduced amino acid sequence. The HEL cell sequence matched a previously reported endothelial cell cDNA sequence except for eight nucleotides. Five of these nucleotide differences were silent changes consistent with genetic polymorphisms. The other three differences resulted in changes in the deduced amino acid sequence of GPIIIa; reexamn. of the endothelial cell cDNA sequence in these three areas revealed that it is actually identical to the HEL cell sequence. The virtual identity of the endothelial and HEL cell cDNA sequences provides direct evidence that GPIIIA is a subunit common to cell-adhesion receptors present in more than one cell type. The gene for GPIIIa was localized to chromosome 17, the same chromosome to which the gene for Platelet aggregation requires the binding of adhesive proteins such as ***fibringen*** to the heterodimer of membrane glycoproteins IIb (GBIID) and IIIa (GBIIIa). Human erythroleukemia (HEL) cells synthesize both GPIIb and GPIIIa. Using poly(A+) RNA purified from HEL cells, a cNA library was constructed in the .lambda.gt10 phage vector. This library

TRAE ANSWER 14 OF 14 CAPLUS COPYRIGHT 2004 ACS g

was mapped.

1987:402841 CAPLUS

107:2841

Protein sequence of endothelial glycoprotein IIIa derived from a cDNA clone. Identity with platelet glycoprotein IIIa and similarity to "integrin"

Fitzgerald, Laurence A.; Steiner, Beat; Rall, Stanley C., Jr.; Lo, Shan Phillips, David R.

Cardiovasc. Res. Inst., Univ. California, San Francisco, San Francisco, CA, 94140-0608, USA

Journal of Biological Chemistry (***1987***), 262(9), 3936-9 CODEN: JBCHA3; ISSN: 0021-9258

Journal

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853 English

GP IIIa, including the N-terminal 19 residues. Thus, the endothelial and plattelet forms of GP IIIa are apparently identical. Glycoprotein IIIa consists of (1) a long N-terminal extracellular domain with several potential N-linked glycosylation sites and 4 cysteine-rich tandem repeats; Clearing the hydrophobic transmembrane segment; and (3) a short. Clearing cytoplasmic domain. Glycoprotein IIIa has a 478 amino acid sequence homel, to integrin, a fibronectin receptor from chicken embryo fibroblasts. This homel, suggests that GP IIIa is a member of a family of Platelet membrane glycoprotein (GP) IIIa forms a Ca2+-dependent heterodimer complex with GP IIb. The GP IID-IIIa complex constitutes the ****fibrinogen*** and fibronectin receptor on stimulated plateless. A biochem, and immunol, similar membrane glycoprotein complex is present on endothelial cells. A human umbilical vein endothelial cell cDNA library was screened using oligonucleotide probes designed from peptide sequences obtained from platelet GP IIIa. A cDNA clone was sequenced and found to encode a protein of 84.5 kilodaltons. The translated endothelial cDNA contained 5 sequences that corresponded to peptide sequences in platelet GP IIIa, including the N-terminal 19 residues. Thus, the endothelial and cell-surface adhesion receptors.

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ANSWER 4 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN ABB70490 Protein DGENE New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions:

Venter J C; Adams M; Li P W D; Myers E W
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US 2000-228716P 20000829
                                                                                                                                          Human fibrinogen E-fragment alpha-chain amino acids 1-78.
                                                                                                                                                                      English
2002-062380 [08]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX protein sequence SEQ ID NO:14114.
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Shimkets R A; Leach M D
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ANO14005 protein DEENE
Novel isolated nucleic acid molecule which encodes a fibrinogen E
polypeptide which is useful for treating cancer, diabetic retinopathy,
obesity, hepatitis, pneumonia, glomerulonephritis, asthma and thyroiditis
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Drmanac R T; Liu C; Tang Y T (YSE-N) HYSEQ INC. (HYSE-N) A2 20011011 W0 2001-US6631 20010330 US 2000-540217 20000331
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N-PSDB: AAS84601
Novel human diagnostic protein #20405.
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                                                                                          New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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N-PSDB: ABL03551
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N-PSDB: ABL14593
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zmanac R T; Liu C;

(HYSE-N) HYSEQ INC.

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(SMIK) SMITHKLINE BEECHAM PLC.

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US 2000-200166P 20000427
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DGENE
Isolated polypeptides, which may be peptide hormones, which are identified by high throughput genome-based biology which identifies genes and gene products as therapeutic targets for treatment of diseases such as diabetes and cancer
Agarwal P; Murdoch P R; Rizvi S K; Smith R F; Xiang Z; Kabnick K S; Lai Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSWER 8 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN ABG02222 Protein DGENE DESIGNATION OF MANAGEMENT OF THE PROPERTY OF THE TRANSPORT OF THE
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N-PSDB: AAI67181
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N-PSDB: AAS66409
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2001-639362 [73]
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                                                                                                                                                                                                                                                                                                                                                                                                                          of GSK gene Id 74552.
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Baker K P; Beresin M; Deforge L; Desnoyers L; Filvaroff E; Gao W; Berritsen M E; Goddard A; Godowski P J; Gurney A L; Sherwood S; Smith V; Stewart T A; Tumas D; Watanabe C K; Wood W I; Zhang Z (GETH) GENENTECH INC.	13 OF 36 5 Protein d, secreto RO polypept tides, and	English English 2001-514838 [56] N-PSDB: AAI90985 Human polypeptide SEQ ID NO 24946.	***WO 2001064835 WO 2001-US4927 US 2000-515126 US 2000-577409	Protein DGENE mucleic acids and polypeptides, useful for preventing e.g. leukaemia, inflammation and immune disorde Liu C; Drmanac R T HYSEQ INC.	ANSWER 1	Patent English 2001-611509 [70] N-PSDB: AAH43522 Protease PRTS-11.	-US9441 20010316 -190708P 20010317 -190708P 20000317 -193182P 20000330 -197086P 20000414 -199022P 20000420 -200227P 20000428	d N; Baughn M R; Nguyen D B; Yao M G; Walia N K; He A; tterson C INCYTE GENOMICS INC. 1720-144 GENOMICS INC.	s, comprises novel human proteases (PRTS) and Licky J L; Delegeane A M; Tribouley C M; Khan F A O: Lal P: Borowsky M L; Gandhi A R: Hillman J L;	ANSWER 11 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAB47569 Protein DGENE New nolypoptide for treating gastrointestinal, cardiovascular and	US 2000-200166F 20000427 Patent English 2001-639223 [73] N-PSDB: AA167180 Amino acid sequence of GSK gene Id 74552.	2000-192668P

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                  ANSWER 19 OF 36 DGENE
AAY64866 Protein
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US 1999-156367
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+*+WO 2001023567 A1 20010405
WO 2000-US26664 20000928
US 1999-156367 19990928
                                                                    Human membrane-bound protein-60 (Zsig60).
                                                                                  2001-266161 [27]
N-PSDB: AAD03542
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2001-266161 [27]
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2001-266161 [27]
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2001-266161 [27]
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US 1999-156367
Novel secreted protein 5' expressed sequence tag sequences used
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2000-205983 [18]
N-PSDB: AAZ93039
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US 1998-96815
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US 1998-57719
US 1998-69047
                                                                                                               New fragments of human fibrinogen, useful f
associated with fibrinogen metabolism -
Grieninger G; Applegate D; Stoike-steben L
(NYBL-N) NEW YORK BLOOD CENT INC.
*****O 2000009562 Al 20000224
WO 1999-USI8412 19990812
US 1998-96210 19980812
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2000-205979 [18]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding secreted proteins, which may have e.g. nutritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor
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Human 5' EST related polypeptide SEQ ID NO:1027.
ANSWER 22 OF 36 DGENE
AAB38373 Protein
                                          AlphaE subunit of human fibrinogen.
                                                                                                                                                                                                                     AAY82891 Protein
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AAY94930 Protein
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2000-038446 [03]
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Clark H F;
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New nucleic acid molecules encoding 62 human secreted proteins for

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W0 20000198979 20000406
US 1999-128693 19990426 wo 2000-US7817 US 1999-125537 US 1999-139565 ANSWER 25 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAB19796 Protein

DGENE
Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy -Human cancer, or for use ...
Rosen C A; Ruben S M ANSWER 24 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAB54135 Protein DGENE DGENE New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition 2000-579485 [54] N-PSDB: AAA96498 Amino acid sequence of a human transmembrane protein. disorder, angina and leukaemia - Yue H; Lal P; Tang Y T; Hillman J L; Reddy R; Bandman O; A M; Azimzai Y; Yang J ANSWER 23 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AABI8955 Protein DGENE DGENE thuman transmembrane proteins are used to treat a disease or condition associated with decreased expression of functional HTMP e.g. Tourette's 2000-647418 [62] Human secreted protein encoded by 2000-579444 [54] N-PSDB: AAC98900 English English (HUMA-N) (INCY-N) WO 2000-US11378 (UYNE-N) UNIV NEW JERSEY MEDICINE & DENTISTRY. ***WO 2000066730 A2 20001109 305p Yurchenco P US 1999-124270 WO 2000-US5989 HUMA-N) HUMAN GENOME SCI INC. ***WO 2000055320 A1 20000921 O 2000-US5989 2000308 INCY-N) INCYTE PHARM INC. pancreatic cancer antigen protein sequence SEQ ID NO:587. 20000322 19990322 19990616 19990312 20000428 gene 53 clone HFABG18. Baughn M R; Lu

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US 1999-139198
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US 1999-155945
Patent
                                                          ANSWER 28 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAB19793 Protein
DGENE
Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy -
                                                                                                                                                                                                                                                                                                                                                    Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy -
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N-PSDB: AAA88896
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(UYNE-N) UNIV NEW JERSEY MEDICINE & DENTISTRY.
***WO 20000066730 A2 20001109 305p
WO 2000-US11378 20000428
                                                                                                                                                       Human laminin 2 mature alpha-2 chain.
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2000-687537 [67]
N-PSDB: AAA88891
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Brunken W; Burgeson R E; Champliaud M; Koch M; Olson P
(GEHO) GEN HOSPITAL CORP.
***WO 9919348 Al 19990422
WO 1998-US21391 19981008
US 1997-61609 19971010
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Human laminin 2
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N-PSDB: AAA88892
                                                                                    Purified laminin 12 useful for promoting tissue repair and promoting
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AAY15460 Protei
                                                                                                                                             Human laminin 2 alpha-2 chain.
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                                                            ARRE2244 Protein DGENE

ARRE2249 Protein DGENE

Production of fibrinogen in transgenic mammals - by introducing DNA
segments into the germ line of a non-human mammal and collecting mil
from female progeny.

Dalrymple M A; Foster D C; Garner I; Prunkard D E
(PHAR-N) PHARM PROTEINS LTD.
(ZYMO) ZYMOGENETICS INC.

***WO 9523868 A1 19950908

WO 1995-US2648 19950301
US 1994-206176 19940303
             English
1995-320582 [41]
N-PSDB: AAT03853
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DGENE
New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for the
                                                                                                                                                                                                                                                                    1995-139597 [18]
N-PSDB: AAQ86480 and AAT17419
Merosin major subunit.
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WO 1994-US10730 19940921

US 1993-125077 19930922
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Human fibrinogen A-alpha chain protein.
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AAR71730 Protein
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N-PSDB: AAZ33446
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DE 1998-1011193
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ANSWER 35 OF 36 DGENE AAR60020 Protein

COPYRIGHT 2004 The Thomson Corp on DGENE

TI New hybrid proteins for use in tissue sealing and wound healing - comprising a tissue-binding domain from a protein covalently linked to a crosslinking domain of another protein (OMYZ) Irani M H ***WO 9416085 ZYMOGENETICS INC. 6085 AZ 19940721 2687 19931230

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CR WO 1993-US12687 US 1992-998271 19921230

Fibronectin. 1994-249231 [30] N-PSDB: AAQ70008

11 A L ANSWER 36 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN

AAR56269 peptide DGENE Synthetic peptide(s) and antibodies against fragment E - derived from plasmin-cleaved fibrinogen useful for therapy of disturbances in the fibrinolytic system

Kraus M; Stueber W

DE 1992-4242736 DE 1992-4242736 ***DE 4242736 BEHRINGWERKE AG. 12736 A1 19940623 12736 19921217 12736 19921217

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1994-209452 [26] Peptide corresponding to C-terminal fragment of cleaved fibrinogen.

=> help display
The DISPLAY command is used to view various types of saved and
Current-session information. To use this command, enter DISPLAY and
the name of the item to be displayed. The system will display the
item online. Highlighting characters may be suppressed by adding the

of records in this file, enter HELP FORMAT at an arrow prompt (=>). For information on the display of records using individual fields or groups of fields, enter HELP DFIELDS. For information on how to create a user-defined display format, enter HELP SET FORMAT. For information on how to change the default display format for this file, enter HELP SET DFORMAT. To see the current default display For information on the predefined formats available for the display format for this file, enter DISPLAY SET DFORMAT.

following For more information about the DISPLAY command, HELP commands at an arrow prompt. enter one of the

l V HELP DISPLAY ACC To see the record for a specific Accession Number in a file

HELP DISPLAY ARCHIVE To grant permission to store STN records for the purposes of electronic access by a specified number of users within your worldwide organization

HELP DISPLAY TOLERANCE - To see the tolerance in effect for

numeric fields available in the current

ii V # **∥** ıı V ij II V **!!** ű II V ij # V II V ATEH HELP HELP DISPLAY FORMAT HELP ATEL HELP DISPLAY BROWSE ---- To browse through an answer set without rekeying the DISPLAY command before each HELP DISPLAY SCAN -----HELP DISPLAY REDISTRIBUTE -- To grant permission to redistribute HELP DISPLAY QUERY ----HELP DISPLAY PFAM -----HELP HELP HELP DISPLAY TERM -----HELP DISPLAY SET -----HELP DISPLAY SELECT HELP DISPLAY PRINT ----DISPLAY SAVED DISPLAY L# -----DISPLAY FROM DISPLAY CURRENCY DISPLAY COST DISPLAY CLUSTER DISPLAY HISTORY DISPLAY FIELD ------- To see the commands used in this session To see the status of offline prints requested in this session To see answers from a search 9 F To see the terms extracted To see the SET parameters currently To see the E-number list from a SELECT To scan through an answer set in random specified number of printed or electronic copies of STN records within your worldwide organization a To see the definition of a query To see selective records from specified patent families in an FSORT L-number multiple files To see records from specific files when To see the user-defined display formats To see the user-defined search fields certain files To see the patent currency status of To see the approximate cost of a session To see user-defined and system-defined SmartSELECT EXPAND command order with a predefined display format To list saved items for this loginid the L-number contains records from file clusters answer number SELECT see the E-number list from an EXPAND changed, command or set permanently Ö

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=> help display format
To see a list of user-defined display formats for this loginid, enter
"DISPLAY FORMAT" at an arrow prompt (=>). This will display for each
user-defined format: its name, its definition, and all files for which
it is the current default format. To display the information for
selected formats, enter "DISPLAY FORMAT" followed by a list of
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Patent Information, Keywords, Organism, Sequence Info
                  An, Sequence Information, Feature Table
An, Sequence Information, Feature Table
An, Molecule Type, Title, Description, Keywords
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Patent Family
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The following are valid formats:

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Patent Information
Application Information
Priority Information Document Title Inventor(s) Accession Number An, Title, Abstract, Inventor(s), Patent Assignee(s),
Patent Information, Keywords, Organism, Sequence Information
Same as ALL, Indented Patent Family An, Sequence Information, Feature Table An, Sequence Information, Feature Table An, Molecule Type, Title, Description, F An, Title, Abstract, Inventor(s), Patent Assignee(s), Patent Information, Application Information, Priority Information, Document Type, Language, Other Source Same as BIB, Indented Format Title, Description, Keywords

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US 2000-206132P
US 2000-228716P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANSWER 1 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN ABP07066 Protein DGENE
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N-PSDB: ABN22818
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to 2001-US10836 20010529
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51 Glu-Ser-Cys-Leu-Phe-Ser-Leu-Ile-Gly-Asn-
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71 Leu-Leu-Arg-Tyr-Gly-Gln-Leu-Leu-Glu-Gln-
81 Ser-Arg-His-Ser-Trp-Val-Asn-Thr-Thr-Xxx-
91 Leu-Ile-Thr-Gly-Cys-Thr-Asn-Ala-Ala-Gly-
101 Leu-Leu-Xxx-Val-Gly-Asn-Phe-Gln-Pro-Arg-
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AAO14005 protein DGENE
3 A; 5 R; 5 N; 8 D; 0 B;
                                                                                                                                                                                                                                                                          AAO14005 protein DGENE
Novel isolated nucleic acid molecule which encodes a fibrinogen E
polypeptide which is useful for treating cancer, diabetic retinopathy,
obesity, hepatitis, pneumonia, glomerulonephritis, asthma and thyroiditis
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                                   Human fibrinogen E-fragment alpha-chain amino acids 1-78.
                                                     N-PSDB: AAK98254
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                                                                           2002-062380 [08]
                                                                                          English
                                                                                                            Patent
                                                                                                                                GB 2000-27396
                                                                                                                                                                                                                         (UYSH-N)
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                                                                                                                                                                                                                                             Lewis C; Staton C
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***WO 2001071042 A2 20
WO 2001-US9231 200
US 2000-191637P 200
US 2000-614150 200
                                                                                                                                                                                                                                                                                                                                                                                                English
2001-65860 [75]
N-PSDB: ABL14593
Drosophila melanogaster polypeptide SEQ ID NO 38262.
ABB70490 Protein DOENE
17 A; 11 R; 12 N; 8 D; 0 B; 3 C; 9 Q; 7 E; 0 Z
20 L; 14 K; 8 M; 14 F; 15 P; 15 S; 12 T; 7 W; 12 Y
229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J C; Adams M; Li P W D; Myers
interactions -
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                                                  Ser-Asp-Glu-Met-Gln-Ile-Tyr-Gly-Tyr-Arg-

val-Ala-Tyr-Met-Ser-Asp-Thr-Glu-Phe-Lys-

Phe-Ser-Ala-Gly-Asn-Trp-Ser-Tyr-Ala-Lys-

Glr-Arg-Asp-Phe-Ser-Phe-His-Gly-Gly-Lys-

His-Phe-Ile-Ile-Pro-His-Leu-Glu-Thr-Asn-
                                                                                                                                        Lys-Asn-Ala-Ser-Gln-Phe-Gly-Asp-Tyr-Lys-
Cys-Lys-Val-Ala-Asn-Pro-Leu-Gly-Met-Leu-
Glu-Arg-Val-Ila-Lys-Leu-Arg-Pro-Gly-Pro-
Lys-Pro-Leu-Gly-Pro-Arg-Arg-Phe-Gln-Leu-
Lys-Lys-Leu-Tyr-Thr-Asn-Gly-Phe-Glu-Leu-
Asp-Ile-Gln-Thr-Pro-Arg-Met-Ser-Asn-Val-
                                                                                                                                                                                                                                                                                       Met-Arg-Ala-Gln-Lys-His-Lys-Pro-His-Trp-
Phe-Phe-Asn-Gln-Thr-Lou-Pro-Val-Gln-Tyr-
Ala-Tyr-Val-Gly-Gly-Ala-Val-Asn-Leu-Ser-
Cys-Asp-Ala-Met-Gly-Glu-Pro-Pro-Pro-Ser-
Phe-Thr-Trp-Lou-His-Asn-Asn-Lys-Gly-Ilo-
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Glu-Gly-Gly-Gly-Val-Arg-Gly-Pro-Arg-Val-
Val-Glu-Arg-His-Gln-Ser-Ala-Cys-Lys-Asp-
Val-Glu-Arg-Pro-Phe-Cys-Ser-Asp-Glu-Asp-
Ser-Asp-Trp-Pro-Phe-Cys-Ser-Asp-Glu-Asp-
               Thr-Thr-Tyr-Leu-Met-Arg-Ala-Ala-Ser-Arg-Asn-Leu-Ala-Gly-Leu-Ser-Asp-Trp-Ser-Pro-
                                                                                                                                                                                                                                                        Asp-Tyr-Gly-Ala-Thr-Leu-Gln-Leu-Gln-Met-
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2 W; 2

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125
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Interactions -
Venter J C; Adams M; Li P W D; Myers E W
(PEKE) PE CORP NY.

***WO 2001071042 AZ 20010927
WO 2001-US9231 20010323
AI US 2000-191637P 2000323
AI US 2000-614150 20000711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB: ABL03551
Drosephila melanogaster p
ABB59446 Protein D
24 A; 26 R; 23 N; 21 D; 0
57 L; 21 K; 10 M; 31 F; 2
438
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AT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
2001-656860 [75]
 Ser-Trp-Ser-Pro-Trp-Leu-Tyr-Pro-Ser-Tyr-
=== === === === === === === === ely-Leu-Ile-Leu-Ala-Leu-Ile-Trp-Thr
210-217
                                                              Phe-Leu-Gly-Gly-Gln-Phe-Leu-Thr-Leu-Gly-
Pro-His-Ala-Leu-Lys-Asn-Arg-Trp-Ser-Asp-
Glu-Leu-Ser-Val-Leu-Asp-Leu-Val-Phe-Pro-
Lys-Ile-Thr-Lys-Cys-Lys-Phe-His-Lys-Phe-
Lys-Ile-Thr-Lys-Cys-Lys-Phe-His-Lys-Phe-
                                                                                                                                                  Ser-Leu-Arg-Ile-Gly-Lys-Leu-Asn-Ile-Pro-
Ser-Yet-Ala-Glu-Ala-Glu-Glu-Arg-Val-Lys-
Asp-Ile-Arg-Arg-Thr-Met-Ile-Asp-Arg-Met-
Arg-Leu-Asn-Gln-Ser-Trp-Gly-Ala-His-Leu-
Val-Phe-Ala-Glu-Val-Leu-Asn-Leu-Ile-Asn-
Val-Phe-Ala-Glu-Val-Leu-Asn-Leu-Ile-Asn-
                                                                                                                                                                                                                                                                                                                                          Phe-Phe-Thr-Pro-Thr-Phe-Thr-Val-Val-Arg-
Asp-Gln-Asn-Gln-Thr-Ala-Tyr-Arg-Pro-Gly-
Ser-Glu-Pro-Pro-Gly-Ile-Gly-Ala-Phe-Asp-
                                                                                                                                                                                                                                                                                                                                                                                             Gly-Glu-His-Ile-Gln-Cys-Leu-Ser-Asp-Gly-Val-Val-Ser-Pro-Val-Ile-Asn-Thr-Phe-Cys-
                                                                                                                                                                                                                                                                                                                                                                                                                              Met-Leu-Asn-Thr-Phe-Ser-Ser-Val-Arg-Gln-
Tyr-Leu-Lys-Phe-Asp-Leu-Thr-Arg-Val-Val-
Ile-Asp-Asn-Ile-Val-Phe-Lys-Leu-His-Tyr-
Arg-Trp-Thr-Phe-Val-Ile-Leu-Leu-Val-Ala-
Thr-Leu-Leu-Lle-Thr-Ser-Arg-Gln-Tyr-Ile-
Gly-Asp-Ser-Gly-Ser-Ile-Gln-Met-His-Asp-
Ala-Leu-Cys-Val-Met-Ala-Leu-Asn-Glu-Lys-Ile-Ile-Leu-Ep-Phe-
Asn-Glu-Lys-Ile-Tyr-Ile-Ile-Leu-Trp-Phe-
Trp-Tyr-Ala-Phe-Leu-Leu-Ile-Val-Thr Val-
                                                                                                                                                                                                                                                        Ala-Leu-Trp-Lys-Ser-Trp-Glu-Gly-Gly-Arg-
Ile-Lys-Ala-Leu-Val-Phe-Gly-Leu-Arg-Met-
                                                                                                                                                                                                                                                                                                         Pro-Glu-Lys-Asp-Thr-Ile-Lys-Arg-His-Ala-
Tyr-Tyr-Gln-Trp-Val-Pro-Phe-Val-Leu-Phe-
                                                                                                                                                                                                                                         Val-Gly-Leu-Thr-Arg-Tyr-Leu-Lys-Asn-Asp-
                                                                                                                                                                                                                                                                                           Phe-Gln-Ala-Leu-Cys-Phe-Tyr-Ile-Pro-His-
                                                                                                                                     Leu-Leu-Leu-Gln-Ile-Thr-Trp-Thr-Asn-Arg-
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DGENE
; 0 B; 7 C; 1
; 22 P; 25 S; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
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V; 0 Others
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English
2001-639362 [73]
N-PSDB: AAS84601
                                                                                                                                                                                                                                                                                                                                                                                         WO 2001-US8631
US.2000-540217
US 2000-649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSWER 6 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN ABG20414 Protein DGENE
New isolated polymuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
DTMADAGER T, LIU C, Tang Y T
                                                                                                                                                                                                                                                                ABG20414 Protein DGENE 204A; 168R; 161N; 180D; 0 B; 164C; 127Q; 202E; 0 Z; 261G; 73 H; 166I; 247L; 189K; 48 M; 102F; 184P; 198S; 191T; 32 W; 93 Y; 152V; 8 Others 3150
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***WO 2001075067
                    Leu-Ser-Gly-Leu-Asp-Thr-Ile-Asp-Ser-Pro-
Leu-Leu-His-Leu-Arg-Arg-Asn-Gly-Ser-Pro-
Ser-Ala-Gly-Gly-Ala-Gln-Gly-Pro-Ser-Thr-
Ser-Asp-Met-Ala-Lys-Leu-Pro-Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leu-Phe-Phe-Leu-Arg-Ser-Asn-Leu-Ser-Glu-
Phe-Lleu-Phe-Llys-Llys-Val-Ile-Tyr-His-Leu-
Ala-Ser-Glu-Phe-Pro-Asn-Pro-Asp-His-Asp-
Asn-Asp-Val-Asn-Ala-Tyr-Arg-Glu-Ala-Pro-
Pro-Thr-Pro-Ala-Lys-Asn-Arg-Tyr-Pro-Glu-
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Cys-Phe-Tyr-Arg-Asn-Val-Thr-Phe-Thr-Arg-
Trp-Ser-Leu-Tyr-Trp-Ala-Lys-Pro-Gly-Gln-
Leu-Asp-Glu-Asn-Glu-Leu-Leu-Ala-Val-Ile-
Asp-Lys-Cys-Asn-Phe-Ser-Asn-Trp-Met-Phe-
Asn-Ser-Pro-Arg-Pro-Gly-Asn-Trp-Ile-Leu-Glu-Arg-Ser-Leu-Asp-Asp-Val-Glu-Tyr-Lys-
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331 Cys-Gly-Asp-Ser-Cys-Asp-Gln-Cys-Cys-Pro-
331 Gys-Gly-Asp-Ser-Cys-Asp-Gln-Cys-Cys-Pro-
341 Gly-Phe-His-Gln-Lys-Thr-Glu-Cys-Glu-Ala-
351 Thr-Phe-Leu-Thr-Lys-Thr-Glu-Cys-Glu-Ala-
361 Cys-Asn-Cys-His-Gly-Lys-Thr-Glu-Cys-Glu-Ala-
361 Cys-Asn-Cys-His-Gly-Lys-Thr-Gln-Cys-Gly-Cys-Gly-Cys-Thr-Gln-
361 Leu-Ser-Leu-Asn-1le-Asp-Cys-Gly-Thr-Gln-
361 Ly-Gly-Gly-Phe-Phe-Arg-Pro-Lys-Gly-Val-
461 Arg-Arg-Gly-Phe-Phe-Arg-Pro-Cys-Gln-Pro-
461 Cys-His-Cys-Asp-Fro-1le-Gly-Ser-Cys-His-
461 Cys-Lys-Thr-Gly-Phe-Gly-Gly-Val-Ser-Cys-His-
461 Cys-Lys-Thr-Gly-Phe-Gly-Cys-Lys-Ser-Gly-Val-
461 Cys-Lys-Thr-Gly-Phe-Gly-Cys-Lys-Ser-Gly-Phe-
461 Cys-Lys-Thr-Gly-Phe-Gly-Cys-Lys-Ser-Gly-
461 Pro-Asp-Cys-Lys-Asn-Glu-Asp-Pro-Cys-Phe-
461 Cys-Lys-Thr-Gly-Phe-Gly-Ser-Gly-
461 Leu-Gly-Ser-Lys-Asn-Glu-Asp-Pro-Cys-Phe-
461 Ly-Gly-Asp-Cys-Lys-Ser-Gly-
461 Pro-Asp-Cys-Lys-Ser-Gly-Ser-Gly-
461 Leu-Gly-Ser-Lys-Ser-Gly-Ser-Gly-
461 Leu-Gly-Ser-Lys-Ser-Gly-Ser-Gly-
461 Leu-Gly-Ser-Lys-Ser-Gly-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Cys-Lys-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Cys-Lys-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Cys-Lys-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Cys-Lys-Ser-Gly-
461 Cys-Cys-Lys-Ser-Gly-Ser-Ser-Cys-Cys-Lys-Ser-Cys-
461 Cys-Cys-Lys-Ser-Cys-Cys-Lys-Ser-
461 Cys-Cys-Lys-Ser-Cys-Cys-Lys-Ser-
461 Cys-Cys-Lys-Ser-
461 Cys-Cys-L
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251 Glu-Phe-Thr-Ser-Ala-Arg-Tyr-Ile-Arg-Leu-

251 Glu-Phe-Gln-Arg-Ile-Arg-Thr-Leu-Asn-Ala-

261 Arg-Phe-Gln-Arg-Ile-Arg-Thr-Leu-Asp-Pro-

271 Asp-Leu-Met-Met-Phe-Ala-His-Lys-Asp-Pro-

281 Arg-Glu-Ile-Asp-Pro-Ile-Val-Thr-Arg-Arg-

281 Arg-Glu-Yesp-Yesp-Yesp-Pro-Asp-Ile-Ser-Arg-

281 Gly-Gly-Met-Cys-Ile-Cys-Tyr-Gly-His-Ala-

281 Gly-Gly-Met-Cys-Ile-Cys-Tyr-Gly-His-Ala-

281 Arg-Ala-Cys-Pro-Leu-Asp-Pro-Ala-Thr-Asn-

281 Arg-Ala-Cys-Pro-Leu-Asp-Pro-Ala-Thr-Asn-
Leu-Leu-Lys-Glu-Glu-Ser-Phe-Thr-Ile-His-
Gly-Thr-His-Phe-Pro-Val-Arg-Arg-Lys-Glu-
Phe-Met-Thr-Val-Leu-Ala-Asn-Leu-Lys-Arg-
Val-Leu-Leu-Gln-Ile-Thr-Tyr-Ser-Phe-Gly-
Met-Asp-Ala-Ile-Phe-Arg-Leu-Ser-Ser-Val-
Asn-Leu-Glu-Ser-Ala-Val-Ser-Tyr-Pro-Thr-
                                                                                                                                                                                                                                                                                     Glu-Glu-Asp-Thr-Glu-Arg-Val-Leu-Gln-Leu-Met-Ile-Ile-Leu-Glu-Gly-Asn-Asp-Leu-Ser-Ile-Ser-Thr-Ala-Gln-Asp-Glu-Val-Tyr-Leu-
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                                                                                                                                                                                                                                                                                                                                                                                                              Lys-Leu-Pro-Ala-Val-Gly-Gly-Gln-Leu-Thr-Phe-Thr-Ile-Ser-Tyr-Asp-Leu-Glu-Glu-Glu-Glu-
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1301 Ala-Arg-Ile-Iu-Val-Arg-His-Met-Ala-Ala1311 Pro-Lou-Ile-Gly-Gln-Iu-Untr-Arg-His-Ala-Ala1321 Ile-Glu-Met-Thr-Gly-Lys-Glu-Txp-Hys-Tyr1331 Tyr-Gly-Asp-Pro-Arg-Val-His-Arg-Trr1341 Val-Thr-Arg-Glu-Lys-Glu-Txp-Ile-Iu1351 Tyr-Gly-Asp-Pro-Arg-Val-His-Tyr1361 Tyr-Asp-Ile-His-Tyr-Ile-Leu-Ile-Iys-Ala1361 Tyr-Asp-Ile-His-Tyr-Ile-Leu-Ile-Iys-Ala1361 Tyr-Asp-Ile-His-Tyr-Ile-Leu-Ile-Iys-Pro1391 Ile-Ser-Glu-Ile-Ser-Yet-Glu-Yet-Arg-Glu1391 Gln-Gly-Arg-Gly-Thr-Thr-Met-Fro-Gly-Pro1401 Ice-Gly-Tyr-Ser-Gly-Pro-Pro1401 Ice-Gly-Tyr-Ser-Gly-Pro-Pro-Glu-Thr1411 Cys-Leu-Pro-Gly-Phe-Tyr-Arg-Leu-Arg-Ser1421 Gly-His-Ser-Ser-Leu-Cys-Asp-Pro-Glu-Thr1431 Ice-Gly-Tyr-Ser-Gly-Arg-Thr-Pro-Gly-Pro-Thr1441 Gly-His-Ser-Ser-Leu-Cys-Asp-Pro-Glu-Thr1441 Gly-His-Ser-Ser-Leu-Cys-Asp-Pro-Glu-Thr1441 Gly-His-Ser-Ser-Ser-Ann-Ann-Phe-Ser-Pro-Ser1441 Gly-Tyr-Tyr-Gly-Ile-Val-Lys-Gly-Leu-Pro1441 Ice-Gly-Tyr-Tyr-Gly-Ile-Val-Lys-Gly-Leu-Pro1441 Ice-Gly-Tyr-Tyr-Gly-Ile-Val-Lys-Gly-Fro-Ile1441 Cly-Thr-Tyr-Gly-Phe-Cys-Asp-Pro-Gly-Fro-Ile1441 Cly-Thr-Tyr-Gly-Fle-Cys-Ala-Cys-Pro-Ile1441 Cly-Thr-Ser-Ser-Ser-Ann-Ann-Phe-Ser-Pro-Ser1441 Cly-Thr-Ser-Ser-Ser-Ann-Ann-Phe-Ser-Pro-Ser1441 Cly-Thr-Ser-Ser-Ann-Ann-Phe-Ser-Pro-Ser1441 Cly-Thr-Ser-Ser-Ann-Ann-Phe-Ser-Pro-Tyr-Cys1441 Cly-Thr-Cys-Clu-Cys-Asp-Pro-Tyr-Cyr1541 Cys-Gln-Glu-Cys-Dr-Arg-Gly-Tyr-Glu-Cys-Pro1542 Gln-Tyr-Cys-Glu-Cys-Pro-Gly-Tyr-Gly-Ser1543 Cys-Gln-Glu-Cys-Dr-Arg-Clu-Thr1544 Cys-Gln-Gly-Ser-Pro-Gly-Asp-Pro-Gly-Tyr1554 Gly-Asp-Glu-Cys-Glu-Cys-Asp-Pro-Gly-Tyr1554 Gly-Asp-Glu-Cys-Glu-Cys-Asp-Pro-Gly-Eleu-Ileu1654 Cly-Asp-Leu-Ala-Ann-Glu-Leu-Leu-Thr1657 Cln-Leu-Ala-Arg-Asp-Glu-Leu-Asp-Gly-Glu-Gly-Ser1668 Thr-Gly-Gly-Asp-Ala-Glu-Leu-Asp-Gly-Glu-Gly1679 Asp-Ala-Clu-Ser-Leu-Cly-Fro-Ile-Lys1680 Thr-Gly-Asp-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Glu-Ala-Ala-Clu-Asp-Glu-Ala-Asp-Clu-Ile-Asp-Clu-Ser-Arg-Gly1680 Arg-Leu-Lys-Lys-Lys

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1961
1971
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331 Gly-Leu-Trp-Asn-Phe-Arg-Glu-Lys-Glu-Gly-
341 Asp-Cys-Tys-Gly-Cys-Thr-Val-Ser-Pro-Gln-
351 Val-Glu-Asp-Ser-Glu-Gly-Thr-Ile-Gln-Phe-
351 Asp-Gly-Glu-Gly-Tyr-Ala-Ile-Gly-Gln-Ala-
351 Arg-Pro-Ile-Arg-Trp-Tyr-Pro-Asn-Ile-Ser-
371 Arg-Pro-Ile-Arg-Trp-Tyr-Phe-Ser-
381 Thr-Val-Met-Phe-Lys-Phe-Arg-Thr-Phe-Ser-
391 Ser-Ser-Ala-Leu-Ileu-Met-Tyr-Leu-Ala-Thr-
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171 Cys-Ile-Arg-Thr-Tyr-Lys-Pro-Glu-Ile-Lys-
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181 Lys-Gly-Ser-Tyr-Asn-Asn-Ile-Val-Val-Asn-
191 Val-Lys-Thr-Ala-Val-Ala-Asp-Asn-Leu-Ieu-
191 Val-Lys-Thr-Ala-Val-Ala-Asp-Asn-Leu-Thr-
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191 Phe-Leu-Ala-Ile-Glu-Mer-Arg-Lys-Gly-Ser-Gly-
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231 Val-Ser-Arg-Thr-Gly-Ser-Thr-His-His-Ser-Thr-
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231 Ser-Pro-Pro-Gly-Tyr-Thr-Ile-Leu-Asp-Val-
231 Lau-Thr-Gly-Cyy-Mer-
231 Lau-Thr-Gly-Gly-Tys-Lau-Asp-Ala-
231 Val-Arg-Val-Ile-Thr-Phe-Thr-Gly-Cyy-Mer-
231 Val-Arg-Val-Ile-Thr-Phe-Thr-Gly-Cyy-Mer-
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Ser-Asn-Gln-Asn-His-Asn-Asp-Gly-Lys-Trp-
                     Leu-Thr-Asp-Gly-His-Ile-Lys-Val-Ser-Tyr-Asp-Leu-Gly-Ser-Gly-Met-Ala-Ser-Val-Val-
                                                                           Arg-Asp-Leu-Arg-Asp-Phe-Met-Ser-Val-Glu-
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Asp-Ala-Asp-Ala-Thr-Val-Lys-Asn-Leu-Glu-
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Leu-Gln-Ala-Val-Lys-Asp-Lys-Ala-Arg-Gln-
Ala-Asn-Asp-Thr-Ala-Lys-Asp-Val-Leu-Ala-
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ANSWER 8 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN
ABG02222 Protein

New isolated polympolectide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity

Drmanca R T; Liu C; Tang Y T

(HYSE-N)

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New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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US 2000-540217
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61 Met-Leu-Glu-Ser-Ile-Lys-Ala-Glu-Pro-Gly-
71 Leu-Ala-Ser-Asp-Val-Ille-Ala-Phe-Asp-Gly-
81 Arg-Tyr-Ser-Ser-Leu-Pro-Glu-Thr-Ala-Ser-
91 Thr-Ala-Thr-Thr-Ille-His-Leu-Ille-His-Gly-
101 Gly-Glu-Asp-Pro-Val-Ille-Asp-Leu-Ala-His-
101 Gly-Glu-Asp-Pro-Val-Ille-Asp-Leu-Ille-Ser-
111 Ala-Val-Ala-Ala-Gln-Thr-Leu-Asp-Ille-Val-
1121 Ala-Gly-Gly-Asp-Val-Thr-Leu-Asp-Ille-Val-
1131 Glu-Asp-Illeu-Gly-His-Ala-Ille-Asp-Asp-Arg-
1141 Ser-Met-Gln-Phe-Ala-Leu-Asp-His-Leu-Arg-
1151 Tyr-Thr-Ille-Pro-Lys-His-Tyr-Phe-Asp-Glu-
1161 Ala-Leu-Ser-Gly
71: 33-40
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IS 2000-540217 20000331
IS 2000-649167 20000823
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2001-639362 [73]
N-PSDE: AAS66409
Novel human diagnostic protein #2213.
AB602222 Protein DGEME
21 A; 12 R; 12 N; 10 D; 0 B; 6 C; 13
34 L; 10 K; 4 M; 6 F; 21 P; 29 S; 13
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US 2000-192158P
US 2000-192668P
                                                                                       ANSWER 9 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN
AAG65891 protein DGENE
Isolated polypeptides, which may be peptide hormones, which are
identified by high throughput genome-based biology which identifies genes
and gene products as therapeutic targets for treatment of diseases such
as diabetes and cancer
                                    Agarwal P; Murdoch P R; Rizvi S K; Smith R F; (SMIK) SMITHKLINE BECHAM CORP. (SMIK) SMITHKLINE BECHAM PLC. ***WO 2001072961 A2 20011004
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Tyr-Glu-Ala-Val-Ala-Ser-Pro-Pro-Ala-Ala-
Leu-Val-His-Leu-Cys-His-Glu-Ala-Val-Ser-
                                                                                                                                                                                                              Val-Arg-Asp-Pro-Leu-Gly-Glu-Ala-Ser-Trp-Ala-Pro-Glu-Ser-Gly-Ala-Asp-Val-Glu-Asn-
                                                                                                                                                                                                                                                                             Leu-Val-Thr-Pro-Ser-Ser-Arg-Pro-Leu-Asn-Pro-Leu-Leu-Thr-His-Ile-Gly-Ser-Tyr-
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Lys-Arg-Gln-Lys-Ser-Gly-Arg-Glu-Val-Tyr-
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Gly-Leu-Tyr-Leu-Ser-His-Alà-Leu-Ser-His-
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19226 20010322
192169 20000324
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                                                                            Xiang Z; Kabnick K S; Lai Y
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2001-639223 [73]
N-PSDB: AAI67181
C Amino acid sequence o:
AAG65891 protein
15 A; 5 R; 15 N; 11 D
23 L; 13 K; 7 M; 6 F;
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161 Val-Ile-Ser-Lys-Pro-Gln-Cys-Arg-Asp-Ala-
171 Tyr-Lys-Thr-Tyr-Asn-Ile-Thr-Glu-Asn-Met-
181 Leu-Cys-Val-Gly-Ile-Val-Pro-Gly-Arg-Arg-
191 Gln-Pro-Cys-Lys-Glu-Val-Ser-Ala-Ala-Pro-
191 Gln-Pro-Cys-Lys-Glu-Val-Ser-Ala-Ala-Pro-
201 Ala-Ile-Cys-Asn-Gly-Met-Leu-Gln-Gly-Ile-
211 Leu-Ser-Phe-Ala-Asp-Gly-Cys-Val-Leu-Arg-
221 Ala-Asp-Val-Gly-Ile-Tyr-Ala-Lys-Ile-Phe-
231 Tyr-Tyr-Ile-Pro-Trp-Ile-Glu-Asn-Val-Ile-
                       WO 2001-US9226
US 2000-192158P
US 2000-192668P
US 2000-200166P
                                                                                                                             ANSWER 10 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAG65890 protein

Isolated polypeptides, which may be peptide hormones, which are identified by high throughput genome-based biology which identifies genes and gene products as the appeutic targets for treatment of diseases such as diabetes and cancer

Agarwal P; Murdoch P R; Rizvi S K; Smith R F; Xiang Z; Kabnick K S; Lai Y SMITHKLINE BEECHAW CORP.

SMITHKLINE BEECHAW CORP.

SMITHKLINE BEECHAW PLC.

***WO 2001072961 A2 20011004
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Pro-Tyr-Leu-Val-Tyr-Leu-Lys-Ser-Asp-Tyr-
Leu-Pro-Cys-Ala-Gly-Val-Leu-Lie-His-Pro-
Leu-Trp-Val-Ile-Thr-Ala-Ala-His-Cys-Asn-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ser-Tyr-Asn-Val-Cys-Asp-Ile-Tyr-Lys-Glu-
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                                              SMITHKLINE BEECHAM CORP.
SMITHKLINE BEECHAM PLC.
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F; 16 P; 17 S; 13 T;
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20 V; 0 Others
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PA PI AI PRAI OS OS DESC HITS DESC AN Ħ 12 Z 5 11 Asn-Leu-Thr-Val-Ala-Leu-Ala-Phe-Asn-Pro21 Asp-Tyr-Thr-Val-Ser-Ser-Thr-Pro-Pro-Pro31 Leu-Val-Tyr-Thr-Val-Ser-Ser-Asp-Tyr-Leu-Pro31 Leu-Val-Tyr-Leu-Lys-Ser-Asp-Tyr-Leu-Pro41 Cys-Ala-Gly-Val-Leu-11e-His-Pro-Leu-Trp42 Cys-Ala-Gly-Val-Leu-11e-His-Pro-Leu-Trp43 Cys-Ala-Gly-Val-Leu-11e-Leu-Gly-Val-Thr-11e44 Cys-Ala-Asp-Ser-Asn-Glu-Lys-His-Leu-Gln45 Val-I1e-Gly-Tyr-Glu-Lys-Met-I1e-His-His46 Val-I1e-Gly-Tyr-Glu-Lys-Met-I1e-His-His47 Pro-His-Phe-Ser-Asn-Glu-Lys-Thr-Glu48 Pro-His-Phe-Ser-Val-Thr-Ser-I1e-Asp-His48 Pro-His-Phe-Ser-Val-Thr-I1e-Ser-Glu-Asn48 Asn-Leu-Pro-Tyr-Gln-Thr-I1e-Ser-Glu-Asn48 Asn-Leu-Pro-Tyr-Gln-Thr-I1e-Ser-Glu-Pro-Asp48 Asn-Leu-Gln-Thr-Val-Asn-I1e-Ser-Val-I1e48 Asn-Val-Cys-Asp-I1e-Tyr-Lys-Glu-Pro-Asp48 Asn-Val-Cys-Asp-I1e-Tyr-Lys-Glu-Pro-Asp49 Cys-Lys-Pro-Gln-Cys-Asp-Asp-Ala-Tyr-Lys40 Cys-Lys-Glu-Val-Ser-Ala-Pro-Ala-I1e40 Cys-Lys-Glu-Val-Ser-Ala-Pro-Ala-I1e40 Cys-Lys-Glu-Val-Ser-Ala-Pro-Ala-I1e40 Cys-Lys-Glu-Val-Ser-Ala-Pro-Ala-I1e40 Cys-Lys-Glu-Val-Ser-Ala-Pro-Ala-I1e40 Cys-Lys-Glu-Val-Ser-Ala-Pro-Ala-I1e41 Asn-Asp-Gly-Tie-Tyr-Ala-Leu-Asp42 Val-Gly-I1e-Tyr-Gly-Asp-Ala-Pro43 Thr-Tyr-Asn-Gly-Asp-Ala-Pro44 Asn-Val-Ser-Ala-Leu-Asp-Ala-Asp44 Asn-Val-Gly-I1e-Gly-Asp-Ala-Asp44 Asn-Val-Gly-I1e-Gly-Asp45 Cys-Lys-Glu-Val-Ser-Ala-Leu-Asp46 Cys-Lys-Gly-Cys-Val-Leu-Asp47 Asn-Gly-I1e-Tyr-Ala-Leu-Asp47 Asn-Gly-I1e-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-I1e-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-I1e-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-I1e-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-I1e-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn48 Asn49 Cys-Lys-Glu-Val-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Gly-Mal-Glu-Asn-Val-I1e-Gln-Asn47 Asn-Glu-Mal-Glu-Asn-Val-I1e-Glu-Asn47 Asn-Glu-Mal-Glu-Asn-Val-I1e-Glu-Asn47 Asn N-PSDB: AA167180

SC Amino acid sequence of GSK gene Id 74
AAG65890 protein DGENE
16 A; 5 R; 15 N; 11 D; 0 B; 9 C; 7
25 L; 13 K; 6 M; 5 F; 15 P; 15 S; 11
241 (INCY-N) INCYTE G

***wo 2001/71004 A

wo 2001-USG441

US 2000-190708P

US 2000-197086P

US 2000-199022P

US 2000-200227P

Patent
English
2001-611509 [70]
N-PSDB: AN43522 polymicleotides Yue H; Lu D A M; Policky J L; Delegeane A M; Tribouley C M; Khan F A;
Au-Young J; Bandman O; Lal P; Borowsky M L; Gandhi A R; Hillman J L; Tang
Y T; Burford N; Baughn M R; Nguyen D B; Yao M G; Walia N K; He A; Hafalia
A; Lu Y; Patterson C
A; Lu Y; Patterson C ANSWER 11 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on SIN AAB47569 Protein DGENE
New polypeptide for treating gastrointestinal, cardiovascular and autoimmune disorders, comprises novel human proteases (PRTS) and 1 11 21 31 41 51 61 61 71 81 91 101 111 121 131 Met-Lys-Phe-Ile-Leu-Leu-Trp-Ala-Leu-Leu-E GENOMICS INC.
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20010316
20000317
20000330
20000420
20000420 C; 7 Q; 5 S; 13 T; 74552. **4** 4 ₹ # 14 , z 20 < છ 7 H; 23 Į,

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Mcdified-site | 11 | 1abel | Active-site | 13.77 | 1abel | 15.54 | 1abel | 10.54 | 1abel | 10.55 | 1abel | 10.55 | 1abel | 10.55 | 1abel | 10.55 | 10.55 | 1abel | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.55 | 10.
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11 Asn-Leu-Thr-Val-Sar-Ser-Thr-Pro-Pro-Tyr-
21 Asp-Tyr-Thr-Val-Ser-Ser-Thr-Pro-Pro-Tyr-
21 Asp-Tyr-Thr-Val-Ser-Ser-Thr-Pro-Pro-Tyr-
31 Leu-Val-Tyr-Leu-Lys-Ser-Asp-Tyr-Leu-Pro-
41 Cys-Ala-Gly-Val-Leu-Ile-His-Pro-Leu-Trp-
51 Val-Ile-Thr-Ala-Ala-His-Cys-Asn-Leu-Pro-
61 Lys-Leu-Arg-Val-Ile-Leu-Gly-Val-Thr-Ile-Pro-
61 Lys-Leu-Arg-Val-Ile-Leu-Gly-Val-Thr-Ile-Pro-
61 Lys-Leu-Arg-Val-Ile-Leu-Gly-Val-Thr-Ile-His-His-
61 Val-Ile-Gly-Tyr-Clu-Lys-Met-Ile-Asp-His-
62 Pro-His-Pho-Ser-Val-Thr-Ser-Ile-Asp-His-
63 Pro-His-Pho-Ser-Val-Thr-Fro-Ser-Glu-Ala-
64 Nash-Ile-Pro-Tyr-Clu-Thr-Ser-Ile-Asp-His-
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66 Ind-Glu-Leu-Asn-Asp-Tyr-Tyr-Tyr-Ser-Tyr-
67 Ile-Phe-Ser-Leu-Asp-Lys-Glu-Pro-Asp-His-
68 Ile-Phe-Ser-Leu-Asp-Lys-Glu-Pro-Asp-Ser-
69 Ile-Phe-Ser-Leu-Asp-Ile-Ser-Val-Ile-Ser-
60 Ile-Glu-Val-Pro-Glu-Asn-Met-Leu-Cys-Val-
61 Ile-Glu-Val-Pro-Glu-Asn-Met-Leu-Cys-Val-
62 Ile-Glu-Val-Pro-Gly-Arg-Arg-Gln-Pro-Cys-
63 Ile-Phe-Ser-Ala-Asp-Ala-Ile-Cys-
64 Ile-Ser-Val-Ile-Ile-Ser-Phe-
65 Ile-Gly-Met-Leu-Cys-Yag-Ala-Asp-Val-
66 Ile-Gly-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
67 Ile-Gly-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
68 Ile-Phe-Ser-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
69 Pro-Trp-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
60 Pro-Trp-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
60 Pro-Trp-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
60 Pro-Trp-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
61 Pro-Trp-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
62 Pro-Trp-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
63 Pro-Trp-Ile-Glu-Asn-Val-Ile-Gln-Asn-Asn
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Potential signal peptide
Potential glycosylation site
Serine protease active site
Type I fibromettin domain
Trypsin domain
Kringle domain
Irypsin active site motif
Potential phosphorylation site
Potential phosphorylation site
Potential phosphorylation site
Potential phosphorylation site
Potential glycosylation site
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ANSWER 12 OF 36 I AAO11054 Protein

DGENE

COPYRIGHT 2004 The Thomson Corp DGENE

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9 Protein R; 15 N; 12 | 3 K; 6 M; 6 |

.i. Ö DGENE 0 B; 15 P;

18 S C 7 14 H (0 4 9 ខ្ម 13 × 53 10 <u>્</u> 0 7 H; 24

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61 Thr-His-Thr-His-Thr-His-Thr-His-
71 Thr-Gly-Leu-Gly-Thr-Gly-Thr-His-
71 Thr-Gly-Leu-Gly-Gly-Gly-Gly-Trp-Gly-Trp-Leu-
81 Gly-Lys-Gln-Ser-Gly-Gly-Trp-Gly-Trp-Leu-
91 Ser-Ala-Asn-Arg-Gly-Glr-Phe-Ser-Pro-Phe-
101 Ala-Val-Cys-Leu-Val-Val-Ser-Phe-Leu-Pro-
111 Glu-Val-Pro-Val-Val-Thr-Ser-Ala-Leu-Phe-
112 Thr
(GETH)

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GENENTECH INC.

***NO 201040466 A2 20010607

W0 2000-US32678 2001201

W0 1999-US28501 19991201

W0 1999-US2851 19991202

W0 1999-US28554 19991202

W0 1999-US28556 19991202

W0 1999-US28565 19991202

W0 1999-US30095 19991216

W0 1999-US30095 19991210

W0 1999-US30999 19991230

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2001-514838 [56]
N-PSDB: AAI90985
                                                                                                                                                                                                                                                                                                                                                                                                            ANSWER 13 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN ANUL295 Protein

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, and detect the presence of mammalian tumours e.g. lung, polypeptides, lung, lung, polypeptides, lung, polypeptides, lung, polypeptides, lung, lung, polypeptides, lung, lung, polypeptides, lung, lung, polypeptides
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AAO11054 Protein DGENE
6 A; 6 R; 2 N; 3 D; 0 B; 4 C;
16 L; 3 K; 1 M; 6 F; 7 P; 12 S;
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                                        141 Asn-Val-Cys-Asp-Ile-Tyr-Lys-Glu-Pro-Asp-
151 Ser-Lys-Pro-Gln-Thr-Val-Asn-Ile-Ser-Val-Ile-
151 Ser-Lys-Pro-Gln-Cys-Arg-Asp-Ala-Tyr-Lys-
151 Ser-Lys-Pro-Gln-Cys-Arg-Arg-Gln-Pro-
171 Thr-Tyr-Asn-Ile-Thr-Glu-Asn-Met-Leu-Cys-
171 Thr-Tyr-Asn-Ile-Pro-Gly-Arg-Arg-Gln-Pro-
171 Thr-Tyr-Asn-Ile-Pro-Gly-Arg-Arg-Gln-Pro-
171 Cys-Lys-Glu-Val-Ser-Ala-Ala-Pro-Ala-Ile-
172 Cys-Lys-Gly-Cys-Val-Leu-Arg-Ala-Asp-
172 Cys-Asn-Gly-Met-Leu-Gln-Gly-Ile-Leu-Ser-
173 Cys-Asn-Gly-Met-Leu-Sin-Leu-Arg-Ala-Asp-
174 Cys-Tile-Tyr-Tyr-Ile-Tyr-Tyr-Tyr-
175 Cys-Tys-Gly-Cys-Val-Lys-Tile-Pho-Tyr-Tyr-
175 Cys-Tys-Gly-Cys-Val-Lys-Tile-Pho-Tyr-Tyr-
175 Cys-Tys-Gly-Cys-Val-Lys-Tile-Pho-Tyr-Tyr-
175 Cys-Tys-Gly-Cys-Tyr-Val-Ile-Gln-Asn-
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Asn-Leu-firr-Val-Ala-Leu-Ala-Phe-Asn-Pro-
Asp-Tyr-Thr-Val-Ser-Ser-Thr-Pro-Pro-Tyr-
Leu-Val-Tyr-Leu-Lys-Ser-Asp-Tyr-Leu-Pro-
Cys-Ala-Gly-Val-Leu-Ile-His-Pro-Leu-Trp-
Val-Ile-Thr-Ala-Ala-His-Cys-Asn-Leu-Pro-
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Asn-Leu-bro-Tyr-Gln-Thr-Ile-Ser-Glu-Asn-
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Pro-Ala-Asp-Ser-Asm-Glu-Lys-His-Leu-Gli-
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163 AAE00333 Protein DGENE Novel membrane bound protein, Zsig60 isolated from pituitary gland, and anti-Zsig60 antibodies which are useful for identifying or isolating cells of pituitary gland and to detect size and morphology of the gland presnell S R (ZYMO) ZYMOGENETICS INC. ***WO 2001023567 A1 20010405 WO 2000-US26664 20000928 US 1999-156367 19990928 Human membrane-bound protein-60 alternative mature AAE00334 Protein DGEME 17 A; 4 R; 7 N; 5 D; 0 B; 10 C; 5 Q; 5 E; 0 20 L; 2 K; 4 M; 5 F; 10 P; 10 S; 8 T; 3 W; 7 160 31 41 51 61 71 71 101 111 1121 121 131 141 151 English 2001-266161 [27] Novel membrane bound protein, Zsig60 isolated from pituitary gland, and anti-Zsig60 antibodies which are useful for identifying or isolating cells of pituitary gland and to detect size and morphology of the gland presnell S 2001-266161 [27] ANSWER 15 OF 36 ZYMOGENETICS INC. ***WO 2001023567 A1 20010405 WO 2000-US26664 20000928 US 1999-156367 19990928 51 Cys-Gly-Ser-Tyr-Pro-Pro-Clu-Ser-Cys-Leu-Gly-Ren-Her-Gly-Ala-Leu-Ile-Cys-Ren-Met-Cy-Ala-Phe-Gly-Ala-Leu-Ile-Cys-Leu-Leu-Arg-Tyr-Bl Gly-Gln-Leu-Leu-Glu-Gln-Ser-Arg-His-Ser-Bl Gly-Gln-Leu-Leu-Glu-Gln-Ser-Arg-His-Ser-Bl Gly-Gln-Ala-Thr-Ala-Leu-Ileu-Thr-Gly-Ill Gly-Asn-Phe-Gln-Val-Asp-His-Ala-Arg-Ser-Ill Gly-Asn-Phe-Gln-Val-Ala-Gly-Val-Ala-Phe-Ill Gly-Asn-Phe-Gly-Ala-Gly-Ala-Cys-Leu-His-Tyr-Val-Gly-Ala-Gly-Val-Ala-Phe-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-His-Ill Gly-Ala-Gly-Leu-Ala-Gly-Ala-Gl 111 21 Ile-Thr-Gly-Ile-Trp-Thr-Val-Tyr-Ala-Met-Ala-Glu-Gln-Gly-Gly-Pro-Lys-Thr-Cys-Cys-Ile-Trp-Thr-Val-Tyr-Ala-Met-Ala-Val-Met-Thr-Leu-Asp-Asp-Val-Pro-Leu-Ile-Ser-Lys-Ser-Tyr-Asn-Glu-Ser-Cys-Pro-Pro-Asp-Pro-Asn-His-His-Val-Cys-Pro-Val-Glu-Asn-Trp-DGENE D; 0 B; 10 C F; 10 P; 10 S protein-60 (Zsig60) mature extracellular COPYRIGHT DGENE DGENE s c 2004 The Thomson Corp on 95 90 ωσ ≋ ლ 70 Υ, ¥; extracellular portion. 14 14 13 G; 6 H; 5 14 V; 0 Others < છ STN 0 0 H; 6 Others Į, H

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41 Thr-Cys-Cys-Thr-Leu-Asp-Asp-Val-Pro-Lou-
51 11e-Ser-Lys-Cys-Gly-Ser-Tyr-Pro-Pro-Glu-
51 11e-Ser-Lys-Cys-Gly-Ser-Tyr-Pro-Pro-Glu-
61 Ser-Cys-Leu-Pho-Ser-Leu-Ile-Gly-Asp-Met-
71 Gly-Ala-Phe-Met-Val-Ala-Leu-Ile-Gly-Ser-Met-
71 Gly-Ala-Phe-Met-Val-Ala-Leu-Glu-Gln-Ser-
81 Leu-Arg-Tyr-Gly-Gln-Leu-Leu-Glu-Gln-Ser-
91 Arg-His-Ser-Trp-Val-Asn-Thr-Thr-Ala-Leu-
101 Ile-Thr-Gly-Cys-Thr-Asn-Ala-Ala-Gly-Leu-
110 Ile-Thr-Gly-Cys-Thr-Asn-Ha-Ala-Gly-Leu-
111 Leu-Val-Val-Gly-Asn-Phe-Gln-Val-Asp-His-
121 Ala-Arg-Ser-Leu-His-Tyr-Val-Gly-Ala-Gly-
131 Val-Ala-Phe-Pro-Ala-Gly-Leu-Phe-Val-
141 Cys-Leu-His-Cys-Ala-Ibu-Ser-Tyr-Gln-Gly-
151 Ala-Thr-Ala-Pro-Leu-Asp-Leu-Ala-Val-Ala-
161 Tyr-Leu-Arg
173 Al: 18-25
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41 Thr-Leu-Asp-Asp-Val-Pro-Leu-Ile-Ser-Lys-
51 Cys-Gly-Ser-Tyr-Pro-Pro-Glu-Ser-Cys-Leu-
61 Phe-Ser-Leu-Ile-Gly-Asn-Met-Gly-Ala-Phe-
61 Phe-Ser-Leu-Ile-Gly-Asn-Met-Gly-Ala-Phe-
61 Met-Val-Ala-Leu-Ile-Cys-Leu-Leu-Arg-Tyr-
81 Gly-Gln-Leu-Leu-Glu-Gln-Ser-Arg-His-Ser-
91 Txp-Val-Asn-Thr-Thr-Ala-Leu-Ile-Thr-Gly-
101 Cys-Thr-Asn-Ala-Ala-Gly-Leu-Val-Val-
111 Gly-Asn-Phe-Gln-Val-Asp-His-Ala-Arg-Ser-
111 Gly-Asn-Phe-Gln-Val-Asp-His-Ala-Arg-Ser-
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27 A; 5 R; 8 N; 7 D; 0 B; 14 C; 8 Q; 9 E; 0 Z; 20 G; 9 H; 30 L; 3 K; 5 M; 11 F; 13 P; 24 S; 14 T; 4 W; 9 Y; 23 V; 0 Oth 256
  AAE00331 Protein DGENE Novel membrane bound protein, Zsig60 isolated from pituitary gland, and anti-Zsig60 antibodies which are useful for identifying or isolating cells of pituitary gland and to detect size and morphology of the gland presnell S \rm R
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                                                                              Cys-Leu-His-Cys-Ala-Leu-Ser-Tyr-Gln-Gly-Ala-Thr-Ala-Pro-Leu-Asp-Leu-Nal-Val-Ala-Tyr-Leu-Arg-Ser-Val-Leu-Ala-Val-Ala-Phe-Ile-Thr-Leu-Val-Leu-Ala-Cys-Gly-Val-Phe-Phe-Val-His-Glu-Ser-Ser-Gly-Leu-Gln-His-Gly-Ala-Ala-Leu-Cys-Glu-Trp-Val-Cys-Val-Gly-Ala-Ala-Leu-Cys-Glu-Trp-Val-Cys-Val-
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Glu-Ser-Ser-Gln-Leu-Gln-His-Gly-Ala-Ala-
Leu-Cys-Glu-Trp-Val-Cys-Val-Tie-Asp-Tie-
                                                                                                                                                                                                                                                                     Ile-Thr-Gly-Cys-Thr-Asn-Ala-Ala-Gly-Leu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glu-Asn-Trp-Ser-Tyr-Asn-Glu-Ser-Cys-Pro-
                                           Ser-Tyr-Glu-Phe-Gly-Ala-Val-Ser-Ser-Asp-
                                                          Ile-Asp-Ile-Leu-Ile-Phe-Tyr-Gly-Thr-Phe-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGENE
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23 V; 0 Others
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2001-266161 [27]
N-PSDB: AAD03542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANSWER 18 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAE00330 Protein DGENE DENE Novel membrane bound protein, Zsig60 isolated from pituitary gland, and anti-Zsig60 antibodies which are useful for identifying or isolating cells of pituitary gland and to detect size and morphology of the gland -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE00330 Protein DGENE
29 A; 5 R; 8 N; 7 D; 0 B; 14 C;
33 L; 3 K; 6 M; 12 F; 14 P; 27 S;
271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human membrane-bound protein-60 (Zsig60).
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***WO 2001023567 A1 20010405
WO 2000-US26664 20000928
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21
31
                                                       91 Leu-Ser-Gly-Val-Phe-Phe-Val-His-Glu-Ser
01 Ser-Gln-Leu-Chn-His-Gly-Ala-Ala-Leu-Cys-
01 Ser-Gln-Leu-Chn-His-Gly-Ala-Ala-Leu-Cys-
11 Glu-Try-Val-Cys-Val-Ile-Asp-Ile-Leu-Ile-
121 Phe-Tyr-Gly-Thr-Phe-Ser-Tyr-Glu-Phe-Gly-
131 Ala-Val-Ser-Ser-Asp-Thr-Leu-Val-Ala-Ala-
141 Leu-Gln-Leu-Pro-Pro-Gly-Azg-Ala-Cys-Lys-
151 Ser-Ser-Gly-Ser-Ser-Thr-Ser-Thr-His-
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18-25
Leu-Asn-Cys-Ala-Pro-Glu-Ser-Ile-Ala-Met-Ile
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Asn-Fhr-Thr-Ala-Leu-Ile-Thr-Gly-Cys-Thr-
Asn-Ala-Ala-Gly-Leu-Leu-Val-Val-Gly-Asn-
Phe-Gln-Val-Asp-His-Ala-Arg-Ser-Leu-His-
Tyr-Val-Gly-Ala-Gly-Val-Ala-Phe-Pro-Ala-
Gly-Leu-Leu-Phe-Val-Cys-Leu-His-Cys-Ala-
                                                                                                                                                                                                                                                                                                                                                                                                                                           Asn-Glu-Ser-Cys-Pro-Pro-Asp-Pro-Ala-Glu-Gln-Gly-Gly-Pro-Lys-Thr-Cys-Cys-Thr-Leu-Asp-Asp-Val-Pro-Leu-Ile-Ser-Lys-Cys-Gly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wat-Thr-Ala-Trp-Ile-Leu-Lou-Pro-Val-Ser-
Leu-Ser-Ala-Phe-Ser-Ile-Thr-Gly-Ile-Thr-
Thr-Val-Tyr-Ala-Met-Ala-Val-Met-Asn-His-
His-Val-Cys-Pro-Val-Glu-Asn-Trp-Ser-Tyr-
                                                                                                                                                                                                                      Leu-Ser-Tyr-Gln-Gly-Ala-Thr-Ala-Pro-Leu-
Asp-Leu-Ala-Val-Ala-Tyr-Leu-Arg-Ser-Val-
                                                                                                                                                                                                                                                                                                                                                                                  Leu-Ile-Gly-Asn-Met-Gly-Ala-Phe-Met-Val-
Ala-Leu-Ile-Cys-Leu-Leu-Arg-Tyr-Gly-Gln-
                                                                                                                                                                                                   Leu-Ala-Val-Ile-Ala-Phe-Ile-Thr-Leu-Val-
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Others
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Key Loc	Location	BLE: Location Qualifier	-
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Peptide	1115	{label	Signal_peptide
Protein	116271	label	Mature_human_Zsig60_protein
Peptide	118	label	Alternative_signal_peptide
Protein	119271	label	Alternative_mature_human_Zsig6
	-	_	10_protein
Region	116178	label	Extracellular_region
Region	119178	label	Alternative_extracellular_regi
	_		on
Region	13956	label	Immunogenic_epitope
Region	3976 label	label	Immunogenic_epitope
Region	39108 label	label	Immunogenic_epitope
Region	[179197]label	label	Membrane_spanning_region
Region	198271 label	label	Intracellular_or_cytoplasmic_r
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AA Patent
English
2000-038446 [03]
N-PSDB: AAA42480
C Human 5' EST related polypeptide SEQ ID
AAY64866 Protein DGEME
3 A; 6 R; 2 N; 0 D; 0 B; 4 C; 1
12 L; 1 K; 2 M; 2 F; 5 P; 10 S; 6 ANSWER 19 OF 36 DGENE UP: ANSWER 19 OF 36 DGENE DEENE DEENE DEENE DEENE DEENE Stephence tag sequences used in Novel Stephence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures Damas Milne Edwards J; Duclert A; Giordano J GENSET. SANSTANDERS WO 1999-IB712 US 1998-57719 US 1998-69047 51 Gly-Ile-His-Glu-Trp-Arg-Pro-Ser-His-Val-61 Cys-Leu-Ser-Cys-Leu-Gly-Ser-Thr-Ser-Cys-71 Asn-Pro-Pro-Glu F: 34-41 11 21 31 41 Tyr-Leu-Leu-Glu-Val-Val-Ala-Pro-Leu-Ser-Met-Ala-Ala-Ser-Val-Leu-Asn-Thr-Val-Leu-: Arg-Arg-Leu-Pro-Met-Leu-Ser-Leu-Phe-Arg-! Gly-Ser-His-Arg-Val-Gln-Val-Thr-Leu-Arg-! Lys-Thr-Phe-Cys-Thr-Thr-Ser-Trp-Leu-19990409 19980409 19980428 ω ⊢ ID NO:1027. 70 Νω € 🖰 -- 0 ¥ 5 Jω < ດ ο ω 3 H; 1) Others Η.

ANSWER 20 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAY94930 Protein DGENE New polynucleotides encoding secreted proteins, which may have e.g. nutritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity -

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DESC AN PA PI AI PRAI H WO 1999-US18298
US 1998-96815
US 1998-96815
US 1998-105368
US 1999-115234
US 1999-120575
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US 1999-13020
US 1999-16622
Patent Jacobs K; Treacy M; Fechtel K Human_secreted protein clone qal36_1 protein AX994930 Protein DGEME
31 A; 19 R; 10 N; 7 D; 0 B; 21 C; 16 Q; 13 48 L; 7 K; 10 M; 16 F; 54 P; 49 S; 21 T; 17 437 English 2000-205979 [18] (GEMY) GENETIC +++WO 2000009552 91 Asn-Glu-Ser-Cys-Pro-Pro-Asp-Pro-Ala-Glu(1) Gln-Gly-Gly-Pro-Lys-Thr-Cys-Cys-Thr-Leu(1) Asp-Asp-Val-Pro-Leu-Ile-Ser-Lys-Cys-Gly(2) Ser-Tyr-Pro-Pro-Glu-Ser-Cys-Leu-Phe-Ser(3) Leu-Ile-Gly-Asn-Met-Gly-Ala-Pye-Gly-Gln(4) Ala-Leu-Ile-Cys-Leu-Bru-Arg-Tyr-Gly-Gln(5) Leu-Leu-Glu-Gln-Ser-Arg-His-Ser-Trp-Val(5) Leu-Leu-Glu-Gln-Ser-Arg-His-Ser-Trp-Val-Thr Txp-Leu-Txp-Pro-Ile-Cys-Glu-Val-CysTxp-Leu-Ser-Pro-Ileu-Ser-Pro-Txp-SerSer-Val-Glu-Ser-Ser-Ieu-Ser-Met-Axg-ValLeu-Ser-Cys-Asn-Met-Gly-Gln-Pro-Cys-ValSer-Gly-Cys-Val-Ser-Ser-Ile-Ser-Ser-Phe-Asn-Thr-Thr-Ala-Leu-Ile-Thr-Gly-Cys-Thr-Asn-Tha-Ala-Gly-Leu-Leu-Val-Val-Gly-Asn-Phe-Gln-Val-Asp-His-Ala-Ala-Ser-Leu-Lala-Phe-Pro-Ala-Tyr-Val-Gly-Ala-Gly-Val-Ala-Phe-Pro-Ala-Gly-Leu-Leu-Phe-Val-Cys-Leu-His-Cys-Leu-Ser-Pro-Thr-Lys-Gly-Pro-Pro-Pro-Arg-Trp-Ser-Pro-Thr-Lys-Gly-Pro-Pro-Pro-Arg-Trp-Leu-Ser-Ala-Phe-Ser-Ile-Thr-Gly-Ile-Trp-Thr-Val-Tyr-Ala-Met-Ala-Val-Met-Asn-His-His-Val-Cys-Pro-Val-Glu-Asn-Trp-Ser-Tyr-Gln-Ser-Pro-Gln-Thr-His-Trp-Trp-Leu-His-Cys-Ser-Leu-Pro-Leu-Ala-Gly-Pro-Ala-Ser-Pro-Pro-Gly-Ala-Ala-Ala-Leu-His-Pro-Pro-Gln-Leu-Cys-Pro-Arg-Glu-His-Arg-Tyr-Asp Ser-Met-Ala-Pro-Ser-Ala-Thr-Ser-Leu-Gly-McCoy J M; LaVallie E R; Collins-Racie L A. Agostino M J; Steininger R J; Spaulding V_i GENETICS INST INC.
100009552 A1 20000224
118298 19990813
1622 19980817
19980817
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19980021
19990218
19990218
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19990218
19990430
19990811 qa136_1 protein sequence SEQ ID NO:66. ₹ F 70 Α, Z; 36 G; 15 H; 13 Y; 27 V; 0 Others Wong G G; Merberg T 0

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English
2000-205983 [18]
N-PSDB: AAZ93039
C AlphaE subunit of human fibrinogen.
AAY92891 Protein
DGRLS
36 A; 53 R; 45 N; 50 D; 0 B; 12 C; 3:
47 L; 43 K; 13 M; 28 F; 41 P; 105S; 5:
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AAY82891 Protein DGENE
New fragments of human fibrinogen, useful for treating conditions associated with fibrinogen metabolism -
Grieninger G, Applegate D, Stoike-steben L
(NYBL-N) NEW YORK BLOOD CENT INC.

***WO 200009562 A1 20000224
WO 1999-US18412 19990812
US 1998-96210 19980812
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111 Val-Ser-Glu-Asp-Leu-Arg-Ser-Arg-11e-Glu-
121 Val-Leu-Lys-Arg-Lys-Val-11e-Glu-
121 Val-Leu-Lys-Arg-Lys-Val-
131 Gln-His-11e-Gln-Leu-Gln-Lys-Asn-Val-
141 Arg-Ala-Gln-Leu-Val-Asp-Met-Lys-Arg-Leu-
141 Arg-Ala-Gln-Leu-Val-Asp-11e-Lys-Arg-Ser-
151 Glu-Val-Asp-11e-Asp-11e-Lys-Trg-Ala-Lu-Ala-
171 Arg-Glu-Val-Asp-Leu-Lys-Asp-Tyr-Glu-Asp-
171 Arg-Glu-Val-Asp-Leu-Lys-Asp-Tyr-Glu-Asp-
171 Arg-Glu-Val-Asp-Leu-Lys-Asp-Tyr-Glu-Asp-
171 Arg-Gln-Lys-Gln-Leu-Glu-Gln-Val-11e-Ala-
181 Gln-Gln-Lys-Gln-Leu-Glu-Glu-Cln-Val-11e-Ala-
182 Gln-Gln-Lys-Gln-Leu-Glu-Glu-Cln-Val-Ala-
183 Gln-Gln-Lys-Gln-Leu-Glu-Glu-Cln-Val-Ala-
184 Gln-Gln-Lys-Gln-Leu-Glu-Glu-Cln-Val-Ala-
185 Gln-Gln-Lys-Gln-Leu-Glu-Glu-Cln-Val-Ala-
185 Gln-Gln-Lys-Gln-Leu-Glu-Glu-Cln-Val-Ala-
185 Gln-Gln-Lys-Gln-Leu-Glu-Gln-Val-I1e-Ala-
185 Gln-Gln-Lys-Gln-Val-I1e-Ala-
185 Gln-Gln-Lys-Gln-Val-I1e-Ala-
185 Gln-Gln-Lys-Gln-Val-IIe-Ala-
185 Gln-Gln-Lys-Gln-Val-IIe-Ala-
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Glu-Gly-Gly-Gly-Val-Arg-Gly-Pro-Arg-Val-
Val-Glu-Arg-His-Gln-Ser-Ala-Cys-Lys-Asp-
Var-Glu-Arg-Pro-Phe-Cys-Ser-Asp-Glu-Asp-
Ser-Asp-Trp-Pro-Phe-Cys-Ser-Asp-Glu-Asp-
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val-Pro-Ser-Thr-Pro-Ser-Ala-Lys-Ala-Arg-
Pro-Leu-Gly-Phe-Pro-Ala-Ala-Gly-Ile-Gly-
Gly-Trp-Glu-Gln-Gln-Arg-Gly
83-90
Lys-Asp-Leu-Leu-Pro-Ser-Arg-Asp-Arg-Gin-
His-Leu-Pro-Leu-Ile-Lys-Met-Lys-Pro-Val-
Pro-Asp-Leu-Val-Pro-Gly-Asn-Phe-Lys-Ser-
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Leu-Pro-Gln-Leu-His-Asp-Leu-Leu-Pro-Thr-
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His-Leurphe-Arg-Thr-Lys-Asn-Asn-Phe-Glu-
Lys-Val-Phe-Cys-Tp-Asp-Leu-Gly-Phe-Leu-
Thr-Ser-Gly-Glu-Val-Ala-Ile-Pro-Cys-Pro-
Thr-Ser-Gly-Glu-Val-Ala-Ile-Pro-Cys-Pro-
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T; 18 W; 24
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4 Y; 41 V; 0 Others
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212 Gly-Thr-Gly-Ser-Thr-Gly-Asn-Gln-Asn-Pro-
313 Gly-Ser-Pro-Aug-Pro-Gly-Ser-Thr-Gly-Thr-
31 Trp-Asn-Pro-Gly-Ser-Ser-Glu-Arg-Gly-Ser-
341 Trp-Asn-Pro-Gly-Ser-Ser-Glu-Arg-Gly-Ser-
351 Ala-Gly-His-Trp-Thr-Ser-Glu-Ser-Ser-Val-
351 Ala-Gly-His-Trp-Thr-Ser-Gly-
351 Ser-Gly-Ser-Phr-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
371 Ser-Gly-Ser-Phe-Arg-Pro-Asp-Ser-Pro-Asp-
371 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
372 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
373 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
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375 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
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370 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
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379 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
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372 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
373 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
374 Ser-Gly-Asn-Ala-Arg-Pro-Asp-Ser-Pro-Asp-
375 Ser-Gly-Asn-Ala-Arg-Pro-Asp-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gly-Gly-Trp-Leu-Leu-Ile-Gln-Gln-Arg-Met-Asp-Gly-Ser-Leu-Asn-Phe-Asn-Arg-Thr-Trp-Gln-Asp-Gly-Ser-Leu-Asn-Asp-Gly-Fer-Leu-Asn-Asp-Gly-Gly-Gly-Fhe-Trp-Leu-Asn-Asp-Gly-Gly-Gly-Gly-Fhe-Trp-Leu-Gly-Asn-Asp-Tyr-Leu-His-Leu-Leu-Thr-Gln-Gly-Asn-Asp-Tyr-Leu-His-Leu-Leu-Thr-Gln-Gly-Asn-Asp-Tyr-Leu-His-Leu-Leu-Thr-Gln-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glu-Ala-Asp-His-Glu-Gly-Thr-His-Ser-Thr-
lys-Arg-Gly-His-Ala-Lys-Ser-Arg-Pro-Val-
Arg-Asp-Gys-Asp-Asp-Val-Leu-Gln-Thr-His-
Pro-Ser-Gly-Thr-Gln-Ser-Gly-Ile-Phe-Asn-
Ile-Lys-Leu-Pro-Gly-Ser-Ser-Lys-Ile-Phe-
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Thr-Ser-Gly-Ser-Thr-Thr-Thr-Arg-Arg
Ser-Cys-Ser-Lys-Thr-Val-Thr-Lys-Thr-Val-
11e-Gly-Pro-Asp-Gly-His-Lys-Glu-Val-Thr-
Lys-Glu-Val-Val-Thr-Ser-Glu-Asp-Gly-Ser-
Asp-Cys-Pro-Glu-Ala-Met-Asp-Leu-Gly-Thr-
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Ala-Leu-Thr-Asp-Met-Pro-Gln-Met-Arg-Met-
Glu-Leu-Glu-Arg-Pro-Gly-Gly-Asn-Glu-Ile-
Thr-Arg-Gly-Gly-Ser-Thr-Ser-Tyr-Gly-Thr-
Arg-Asp-Ala-Asp-Gln-Trp-Glu-Glu-Asn-Cys-Ala-Glu-Val-Tyr-Gly-Gly-Gly-Trp-Trp-Tyr-
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Ser-Tyr-Lys-Met-Ala-Asp-Glu-Ala-Gly-Ser-
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                                                                                                                  His-Asn-Asn-Met-Gln-Phe-Ser-Thr-Phe-Asp-
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2000-579485 [54]
N-PSDB: AAA96498
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AAB38373 Protein

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                                                                                                                                            WO 2000-US7817
US 1999-125537
US 1999-139565
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AAB38373 Protein DGENE
10 A; 1 R; 3 N; 4 D; 0 B; 4 C; 1 Q; 4 E; 0 Z; 6
L; 1 K; 3 N; 1 F; 11 P; 7 S; 5 T; 3 W; 2 Y; 6 V; 88
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801 Ifle-Tyr-Tyr-Pro-Gly-Gly-Ser-Tyr-Asp-Pro-
811 Arg-Asn-Asn-Ser-Pro-Tyr-Glu-Ila-Glu-Asn-
821 Gly-Val-Val-Trp-Val-Ser-Pha-Arg-Gly-Ala-
831 Asp-Tyr-Ser-Leu-Arg-Ala-Val-Arg-Met-Lys-
831 Asp-Tyr-Ser-Leu-Arg-Ala-Val-Arg-Met-Lys-
                                                                                                                                                                                                                                                                                                           ANSWER 23 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN
ABB18985 Protein DGENE
New human transmembrane proteins are used to treat a disease or condition
associated with decreased expression of functional HTMP e.g. Tourette's
disorder, angina and leukaemia -
Yue H; Lal P; Tang Y T; Hillman J L; Reddy R; Bandman O; Baughn M R; Lu D
A M; Azimzai Y; Yang J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ***WO 2000061623 AI 20001019
WO 2000-US8979 20000406
US 1999-128693 19990409
US 1999-130991 19990426
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2000-647418 [62]
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Leu-Ser-Ala-Phe-Ser-Ile-Trp-
Thr-Val-Tyr-Ala-Met-Ala-Val-Met-Asn-His-
His-Val-Cys-Pro-Val-Glu-Asn-Trp-Ser-Tyr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asn-Glu-Ser-Cys-Pro-Pro-Asp-Pro-Ala-Glu-
Gln-Gly-Gly-Pro-Lys-Thr-Cys-Cys-Gys-Thr-Leu-
Asp-Asp-Val-Pro-Leu-Ile-Ser-Gly-Pro-Asp-
Leu-Pro-Pro-Ala-Leu-Arg-Ala-Ala-Pro-Gly-
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6 V; 1 Others
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AAB18985
29 A; 5
32 L; 3
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Ser-Tyr-Pro-Pro-Glu-Ser-Cys-Leu-Phe-Ser-
Leu-Ile-Gly-Asn-Met-Gly-Ala-Phe-Met-Val-
                                                           Ala-Val-Ser-Ser-Asp-Thr-Leu-Val-Ala-Ala-
Leu-Gin-Pro-Thr-Pro-Gly-Arg-Ala-Cys-Lys-
Ser-Ser-Gly-Ser-Ser-Ser-Thr-Ser-Thr-His-
                                                                                                                                                                                                                                             Tyr-Val-Gly-Ala-Gly-Val-Ala-Phe-Pro-Ala-Gly-Leu-Leu-Phe-Val-Cys-Leu-His-Cys-Ala-Leu-Ser-Tyr-Gly-Gly-Ala-Thr-Ala-Pro-Leu-
                                                                                                                                                                                                                                                                                                      Asn-Thr-Thr-Ala-Leu-Ile-Thr-Gly-Cys-Thr-
Asn-Ala-Ala-Gly-Leu-Leu-Val-Val-Gly-Asn-
Phe-Gln-Val-Asp-His-Ala-Arg-Ser-Leu-His-
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Leu-Asn-Cys-Ala-Pro-Glu-Ser-Ile-Ala-Met-
Ile
33~40
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                                                                                                                                                                                                    Asp-Leu-Ala-Val-Ala-Tyr-Leu-Arg-Ser-Val-
Leu-Ala-Val-Ile-Ala-Phe-Ile-Thr-Leu-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gln-Gly-Gly-Pro-Lys-Thr-Cys-Cys-Thr-Leu-
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                                                                                                                         Phe-Tyr-Gly-Thr-Phe-Ser-Tyr-Glu-Phe-Gly-
                                                                                                                                                                                     Leu-Ser-Gly-Val-Phe-Phe-Val-His-Glu-Ser-
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K; 6 M; 12
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D; 0 B; 14 C;
2 F; 14 P; 27 S;
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) Others
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FEATURE TABLE:

HITS

Key IL	Location Qualifier	ifier
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Peptide 1	121 note	"signal peptide"
Modified-site 37	7 (note	"potential glycosylation site"
Modified-site 3	9 (note	_
_		site"
Modified-site 4	1 note	"potential glycosylation site"
Modified-site 5	9 note	_
Modified-site 1	-	<pre> site" "potential glycosylation site"</pre>
Modified-site 37 Modified-site 39 Modified-site 41 Modified-site 59 Modified-site 111	<u>.</u> 	

ANSWER 24 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAB54135 Protein DGENE DENE New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition

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IN PA PA PI AI PRAI DT LA OS CR CR AN AA
                                 HITS
 R L7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
2000-579444 [54]
N-PSDE: AAC98900
Human pancreatic ca
AAB54135 Protein
13 A; 27 R; 20 N; 2
34 L; 27 K; 9 M; 7
360
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US 199
Patent
                                            Rosen C )
(HUMA-N)
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(HUMA-N) HUMAN GENOME SCI INC
(***W0 2000-US5989 20000308
W0 2000-US5989 20000308
US 1999-124270 19990312
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211
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                                                                                      Leu-Asn-Pro-Gly-Arg-Pro-Ala-Arg-Pro-Val-
Leu-Leu-Arg-Ser-Xxx-Ala-Pro-Pro-Leu-Glu-
Lys-Met-Phe-Ser-Met-Arg-Tle-Val-Cys-Leu-
Val-Leu-Ser-Val-Val-Gly-Thr-Ala-Trp-Thr-
Val-Leu-Ser-Val-Val-Gly-Thr-Ala-Trp-Thr-
Ala-Asp-Ser-Gly-Glu-Gly-Asp-Phe-Leu-Ala-
Glu-Gly-Gly-Gly-Gla-Arg-Gly-Pro-Arg-Val-
Val-Glu-Arg-His-Gln-Ser-Ala-Cys-Lys-Asp-
Val-Glu-Arg-His-Gln-Ser-Ala-Cys-Lys-Asp-
                                 Ser-Gly-Thr-Trp-Xxx-Xxx-Xxx-Asn-Leu-Glu-Thr-Trp-Glu-Leu-Trp-Thr-Trp-Lys-Xxx-Trp-Lys-Leu-Glu-Leu-Trp-Glu-Leu-Trp-Asn-Trp-Lys-Tyr-Trp-Lys-Pro-Trp-Glu-Pro 76-83
                                                                                                                                                                                                                                                    Lys-Asp-Ser-His-Ser-Leu-Thr-Thr-Asn-Ile-Wet-Glu-Ile-Leu-Arg-Gly-Asp-Phe-Ser-Ser-Ala-Asn-Asn-Arg-Arg-Arg-Arg-Arg-Clu-Arg-Arg-Arg-Arg-Leu-Arg-Ser-Arg-Ile-Glu-Val-Ser-Glu-Asp-Leu-Arg-Ser-Arg-Ile-Glu-Lys-Val-Clu-His-Ile-Gln-Leu-Leu-Gln-Lys-Asn-Val-Cln-His-Ile-Gln-Leu-Leu-Gln-Lys-Asn-Val-
                                                                                                                                                                                                                                                                                                                        Met-Lys-Gly-Leu-Ile-Asp-Glu-Val-Asn-Gln-
Asp-Phe-Thr-Asn-Arg-Ile-Asn-Lys-Leu-Lys-
Asn-Ser-Leu-Phe-Glu-Tyr-Gln-Lys-Asn-Asn-
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Protein
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n DGENE
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US 1999-143289 19900712
US 1999-143289 19900712
US 1999-155945 1990924
Patent
English
2000-687537 [67]
N-PSDB: AAA88896
SC Wouse laminin 2 mature alpha-2 chain.
AAB19796 Protein
183A; 163R; 164R; 181D; 0 B; 161C; 123Q; 20:
242L; 171K; 43 M; 101F; 175P; 207S; 187T; 27
3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy - Yurchenoo P (UYNE-N) UNIV NEW JERSEY MEDICINE & DENTISTRY.

***WO 2000066730 A2 20001109

305p***
    Gln-Arg-Arg-Gln-Ser-Gln-Ala-His-Gln-Gln-Arg-Gly-Leu-Phe-Pro-Ala-Val-Leu-Ran-Leu-Ala-Ser-Asn-Ala-Deu-Ile-Thr-Thr-Asn-Ala-Thr-Cys-Gly-Glu-Lys-Gly-Pro-Glu-Met-Tyr-Cys-Lys-Leu-Val-Glu-His-Val-Pro-Gly-Gln-Pro-Val-Arg-Asn-Pro-Gln-Cys-Arg-Ile-Cys-Pro-Val-Arg-Asn-Pro-Gln-Cys-Arg-Ile-Cys-
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27 W;
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99 Y; 165V; 0 Others
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Ser-Pro-Val-Pro-Tyr-Pro-Thr-Asp-Arg-Arg-Arg-Arg-Arg-Arg-Arg-Arg-Arg-Arg	17788
<pre>[Glu-Glu-Alla-Phe-Thr-Ile-His-Gly-Thr-As [Laut-Phe-Vall-Thir-Arg-Lys-Asp-Phe-Met-Il [Vall-Leut-Thr-Asn-Leu-Gly-Glu-Ile-Leut] [Gln-Ile-Thr-Tyr-Asn-Leu-Gly-Met-Asp-Al [Ile-Phe-Arg-Lau-Ser-Ser-Val-Asn-Leu-Gl]</pre>	9 9 9 9 9
Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-	561 601 621
Cys-Gin-Ser-Ser-Tyr-Trp-Th ===================================	
r.lle A.y. F. O. Ly S. G.Y. Pro-Arg-Pro-Cys-Gln-Pro-Cys-Gln-Pro-Cys-Gln-Val-Cy-Pro-Thr-Gly-Ser-Ida-Cys-Tyr-Ala-Gln-Arg-Gl-Lys-Ep-Gly-Ng-Tyr-Ala-Gln-Arg-Gl-Lys-Pro-Gly-Gly-Ser-Cys-His-Cys-Lys-Thr-Pro-Arg-Cy-Arg-Gly-Tyr-His-Gly-Flyr-Pro-Arg-Cy-Pro-Cys-Asn-Cys-Ser-Gly-Leu-Gly-Flo-Cys-Lys-Glu-Asp-Pro-Cys-Val-Gly-Pro-Cys-Lys-Glu-Asp-Pro-Cys-Lys-Glu-Glu-Gly-Glu-Asp-Asn-Val-Glu-Gly-Glu-Asp-Gly-Lys-Ser-Gly-Dhe-Phe-Phe-Asn-Glu-Glu-Asp-Asn-Cys-Lys-Glu-Gly-Glu-Asp-Cys-Lys-Gly-Dhe-Phe-Phe-Asn-Cys-Phe-Cys-Lys-Gly-Blu-Asp-Cys-Lys-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly	00000000000000000000000000000000000000
Gly-Ile-Asn-Cys-Glu-Thr-Cys-Val-A	10

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921 His-Cys-Asp-Glu-Cys-Iys-Pro-Glu-Thr-Phe-
931 Gly-Leu-Gln-Isu-Gly-Arg Gly-Cys-Leu-Pro-
941 Cys-Asn-Cys-Asn-Ser-Phe-Gly-Ser-Iys-Ser-
951 Phe-Asp-Cys-Glu-Ala-Ser-Gly-Gln-Cys-Irp-
961 Cys-Gln-Pro-Gly-Val-Ala-Ser-Gly-Gln-Cys-Irp-
962 Gln-Gly-Gln-Pro-Gly-Val-Ala-Gly-Lys-Lys-Cys-
971 Asp-Arg-Cys-Ala-His-Gly-Tyr-Phe-Asn-Phe-
983 Gln-Glu-Gly-Gly-Cys-Ile-Cys-Glu-Cys-Asp-Cys-
984 Gln-Gly-Gly-Cys-Ile-Cys-Fro-Pro-Asn-Thr-
1001 Thr-Gly-Glu-Lys-Cys-Ser-Glu-Cys-Leu-Pro-
1001 Thr-Gly-Glu-Lys-Cys-Ser-Glu-Cys-Leu-Pro-
1001 Gly-Glu-Lys-Cys-Ser-Glu-Cys-Asn-Thr-
1001 Gly-Glu-Lys-Cys-Ser-Glu-Cys-Asn-Thr-
1001 Gly-Met-Lys-Cys-Ser-Glu-Cys-Ser-Arg-Gly-
1001 Ms-Trp-Asn-Tyr-Pro-Leu-Cys-Thr-Leu-Cys-
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1001 Thr-Cys-Asp-Gln-Thr-Gly-Gln-Cys-Ser-Cys-
1101 Cys-Ser-Asp-Gln-Thr-Gly-Gln-Cys-Ser-Cys-
1101 Thr-Cys-Asp-Eu-Clu-Cly-Thr-Asp-Ala-Thr-
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1104 Tyr-Cys-Phe-Gly-Val-Thr-Ser-Gln-Cys-Ser-Cys-
1105 Glu-Ala-Tys-Gly-Ile-Ala-Thr-Ser-Gln-Cys-Ser-Cys-
1107 Thr-Leu-Ser-Asp-Glu-Gln-Thr-Ile-Leu-Pro-
1108 Thr-Leu-Ser-Asp-Glu-Gln-Thr-Ile-Leu-Pro-
1109 Thr-Cys-Asp-Edlu-Cln-Thr-Ile-Leu-Pro-
1109 Thr-Leu-His-Leu-Glu-Thr-Gln-Lys-Thr-Trp-Val-
1109 Thr-Cys-Asp-Clu-Cln-Thr-Ile-Leu-Pro-
1109 Thr-Ala-Tyr-Gly-Ily-Ser-Cys-Glu-Val-Arg-Gln-
1120 Glu-Leu-His-Leu-Glu-Pro-Cln-Val-Arg-Clu-
1221 Leu-Pro-Gln-Gln-Phe-Glu-Vly-Tys-Leu-
1221 Leu-Pro-Gly-Gly-Thr-Pro-Thr-His-Ala-Arg-Thr-Trp-Val-
1221 Leu-Pro-Gly-Thr-Pro-Thr-His-Ala-Arg-Thr-Tyr-Gly-
1221 Asp-Pro-Asg-Gly-Gly-Tys-Tyr-Tyr-Gly-Asp-
1221 Asp-Pro-Asg-Gly-Gly-Tys-Gly-Tyr-Gly-Asp-
1221 Asp-Cys-Chu-Arg-Cys-Pro-Pro-Gly-Thr-
1221 Leu-Pro-Cys-Asp-Cys-Clu-Thr-Cys-Ala-Pro-
1221 Leu-Pro-Cys-Asp-Cys-Pro-Pro-Gly-Thr-
1221 Leu-Pro-Cys-Asp-Cys-Pro-Pro-Gly-Tyr-
1222 Asp-Pro-Cys-Asp-Cys-Pro-Pro-Gly-Tyr-
1223 Asp-Cys-Asp-Cys-Thr-Ala-Cly-Asp-
1224 Thr-Tyr-Tyr-
1225 Thr-Tyr-Tyr-
1226 Thr-Tyr-Tyr-
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701 Glu-Leu-Arg-Ser-Lys-Asp-Leu-Gln-Thr-Gln-
701 Lys-Glu-Val-Ala-Glu-Asp-Glu-Leu-Val-Ala-
711 Lys-Glu-Val-Ala-Glu-Asp-Glu-Leu-Lys-
721 Ala-Glu-Gly-Glu-Pro-Arg-Ala-Gln-Asn-Lys-
731 Leu-Phe-Gly-Glu-Pro-Arg-Ala-Gln-Asn-Glu-
741 Asp-Met-Glu-Lys-Asp-Leu-Gln-Gln-Lys-Leu-
741 Asp-Met-Glu-Lys-Asn-Lys-Leu-Asp-Asp-Ala-
751 Ala-Glu-Tyr-Lys-Asn-Lys-Leu-Asp-Asp-Ala-
761 Trp-Asp-Leu-Leu-Arg-Glu-Ala-Thr-Asp-Lys-
771 Thr-Arg-Asp-Ala-Asn-Arg-Leu-Ser-Ala-Ala-
771 Thr-Arg-Asp-Ala-Asn-Arg-Leu-Ser-Ala-Ala-
781 Asn-Gln-Lys-Asn-Met-Thr-Ile-Lu-Ser-Lys-Arg-
791 Lys-Lys-Glu-Ala-Ile-Glu-Gly-Ser-Lys-Arg-
791 Lys-Lys-Glu-Ala-Thr-Leu-Lys-Glu-Gly-Asn-
791 Lys-Lys-Glu-Asn-Thr-Leu-Lys-Glu-Gly-Asn-
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311 Glu-Gly-Asn-Val-Asn-Thr-Leu-Val-Met-Glu-
321 Thr-Asn-Glu-Ieu-Leu-Thr-Arg-Ala-Thr-Lys-
321 Val-Thr-Ala-Asp-Gly-Glu-Gln-Thr-Gly-Gln-
331 Val-Thr-Ala-Asp-Gly-Glu-Gln-Thr-Gly-Gln-
341 Asp-Ala-Glu-Arg-Thr-Asn-Ser-Arg-Ala-Glu-
351 Ser-Leu-Glu-Glu-Phe-Ile-Lys-Gly-Leu-Val-
351 Ser-Leu-Glu-Glu-Phe-Ile-Lys-Asn-Gln-
351 Val-Lys-Leu-Asn-Glu-Thr-Leu-Gly-Asn-Gln-
351 Val-Lys-Leu-Asn-Glu-Thr-Leu-Gly-Asn-Gln-
351 Val-Lys-Thr-Ala-Glu-Arg-Asn-Leu-Glu-Glu-
352 Asp-Lys-Thr-Ala-Glu-Arg-Asn-Leu-Glu-Glu-
353 Asp-Lys-Thr-Ala-Glu-Arg-Asn-Leu-Glu-Glu-
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Gly-Glu-Ile-Asn-Ser-Val-Ile-Asp-Tyr-Val-
Asp-Asp-Ile-Lys-Thr-Lys-Leu-Pro-Pro-Met-
Ser-Glu-Glu-Leu-Ser-Asp-Lys-Ile-Asp-Asp-
Leu-Ala-Gln-Glu-Ile-Lys-Asp-Axg-Axg-Leu-
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Cys-Asp-Gly-Cys-Glu-His-Trp-His-Ala-Arg-
Glu-Gly-Ala-Glu-Cys-Val-Phe-Cys-Gly-Asp-
Asp-Leu-His-Gln-Asn-Leu-Asp-Gly-Leu-Lys-Gln-Asn-Tyr-Asn-Lys-Leu-Ala-Asp-Ser-Val-Ala-Lys-Thr-Asn-Ala-Val-Val-Lys-Asp-Pro-
                                                                                                            Thr-Asn-Asp-Thr-Ala-Ala-Lys-Leu-Gln-Ala-Val-Lys-Glu-Lys-Ala-Asp-Asp-Glu-Ala-Asn-Asp-Thr-Ala-Lys-Ala-Val-Leu-Ala-Gln-Val-Lys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ala-Glu-Lys-Val-Phe-Gln-Ala-Glu-Ser-His-
Ala-Ala-Gln-Leu-Asn-Asp-Ser-Ser-Ala-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lys-Ile-Leu-Tyr-Gly-Leu-Glu-Asn-Thr-Thr-Gln-Glu-Leu-Lys-His-Leu-Leu-Ser-Pro-Gln-
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291 Asn-Phe-Asp-Asn-Lys-Glu-Gly-Asp-Cys-Lys-
301 Gly-Cys-Thr-Val-Ser-Pro-Gln-Val-Glu-Asp-
301 Gly-Cys-Thr-Val-Ser-Pro-Gln-Val-Glu-Asp-
301 Gly-Tyr-Ala-Leu-Val-Ser-Arg-Pro-11e-Arg-
301 Gly-Tyr-Ala-Leu-Val-Ser-Arg-Pro-11e-Arg-
301 Gly-Tyr-Ala-Leu-Val-Ser-Arg-Pro-11e-Arg-
301 Lys-Phe-Arg-Thr-Phe-Ser-Ser-Ser-Ala-Leu-
401 Lys-Phe-Mer-Ser-Val-Glu-Leu-Ser-Asp-Leu-Lys-
301 Asp-Phe-Mer-Ser-Val-Val-Ser-Asp-Gly-Ser-
301 Als-Phe-Mer-Ser-Val-Val-Ser-Asn-Gln-Asn-
301 His-Val-Lys-Gly-Lys-Trp-Lys-Ala-Phe-Thr-
301 His-Val-Asp-I1e-Gln-Lys-Ser-Asn-Gln-Glu-
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401 Leu-Ser-Asp-Gly-Lys-Trp-Lys-Ala-Asn-
401 Glu-Asn-Val-Ala-Thr-Ser-Ser-Gly-Asn-
401 Glu-Asn-Val-Ala-Thr-Ser-Ser-Gly-Asn-
401 Asn-Phe-Gly-Leu-Asp-I1e-Gln-Lys-Ala-Asp-Asn-
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401 Asn-Phe-Gly-Clys-Lys-Asn-
401 Asn-Phe-Gly-Clys-Lys-Asn-
401 Asn-Phe-Gly-Clys-Clys-Asn-
401 Asn-Phe-Gly-Clys-Clys-Clys-Clys-Clys-Clys-
401 Asn-
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[51 Ala-Val-Ala-Asp-Asn-Leu-Leu-Phe-Tyr-Leu-
[51 Ala-Val-Ala-Asp-Asn-Leu-Leu-Phe-Tyr-Leu-
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Pro-Ser-Thr-Tyr-His-Ser-Val-Ser-Pro-Pro-
Gly-Tyr-Thr-Ile-Leu-Asp-Val-Asp-Ala-Asn-
Ala-Met-Leu-Phe-Val-Gly-Gly-Leu-Thr-Gly-
Lys-Ile-Lys-Lys-Ala-Asp-Ala-Val-Arg-Val-
Ile-Thr-Phe-Thr-Gly-Cys-Met-Gly-Glu-Thr-
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Ser-Val-Ser-Ser-Gly-Gly-Asp-Cys-Val-Arg-
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US 1999-143289
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                                                                                                                                 ANSWER 26 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAB19795 Protein DGENE Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, anglogenesis regulation, and ex vivo cell therapy -
W JERSEY MEDICINE 6
A2 20001109
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19990430
19990615
19990712
19990924
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65 H; 167I; 0 Others

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471 Gly-Ser-Thr-Asn-Glu-Asp-Pro-Cys-Val-Gly-
491 Glu-Asp-Cys-Ser-Cys-Lys-Glu-Asn-Val-Glu-Gly-
491 Glu-Asp-Cys-Ser-Cys-Lys-Gu-Asn-Val-Glu-Gly-
491 Glu-Asp-Cys-Ser-Cys-Lys-Ser-Gly-Phe-
501 Phe-Asn-Leu-Gln-Glu-Asp-Asn-Gln-Lys-Gly-
511 Cys-Glu-Glu-Cys-Phe-Cys-Ger-Cly-Val-Ser-
521 Asn-Arg-Cys-Gln-Ser-Ser-Tyr-Thr-Thr-Tyr-
521 Asn-Arg-Cys-Gln-Ser-Ser-Tyr-Tp-Thr-Tyr-
521 Asn-Arg-Cys-Gln-Ser-Ser-Tyr-Tp-Thr-Tyr-
521 Ala-Pro-Gln-Leu-Asp-Met-Arg-Gly-Tyr-Tyr-
521 Leu-Thr-Asp-Leu-Ser-Gly-Arg-Ile-Asp-Arg-
521 Leu-Pro-Gln-Leu-Asp-Asn-Pro-Asp-Ser-Pro-
521 Leu-Thr-Asp-Leu-Ser-Gly-Arg-Ile-Asp-Arg-
521 Leu-Pro-Pro-Pro-Pro-Tyr-Leu-Glu-Glu-Glu-
621 Thr-Ile-Phe-Glu-Gly-Asn-Asp-Leu-Glu-Glu-Glu-
631 Ser-Thr-Ala-Tyr-Lys-Glu-Glu-Glu-Val-Ser-
631 Ser-Thr-Ala-Tyr-Lys-Glu-Glu-Glu-Val-Ser-
641 Pro-Ser-Glu-Glu-Ala-Pro-Pro-Pro-
651 Leu-Lys-Glu-Glu-Ala-Tyr-Lys-Glu-Glu-Val-Ser-
651 Leu-Lys-Glu-Glu-His-Val-Glu-Glu-Val-Cys-
661 Thr-Asn-Leu-Pro-Val-Thr-Asn-Leu-Gly-Glu-Ile-
661 Leu-Ile-Cln-Ile-Thr-Tyr-Asn-Leu-Gly-Glu-Ile-
661 Leu-Ile-Cln-Ile-Thr-Tyr-Asn-Leu-Gly-Glu-Ile-
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661 Leu-Ile-Cln-Ile-Thr-Tyr-Asn-Leu-Cly-Glu-Ile-
672 Asn-Asp-Pro-Pro-Gly-Tyr-Ser-Gly-Gly-Gly-Ser-Ser-
771 Lan-Gly-Asp-Asp-His-Thr-Gly-Gly-Gly-Gly-Ser-Ser-
771 Lan-Cys-Lys-Asp-His-Thr-Gly-Gly-Gly-Gly-Gly-
771 Asn-Cys-Lys-Asp-His-Thr-Gly-Gly-Gly-Ser-Cys-
771 Asn-Cys-Lys-Asp-His-Thr-Gly-Gly-Gly-Ser-Cys-
771 Asn-Cys-Leu-Ile-Cys-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asn-Asp-Asn-Leu-Asp-Cys-
771 Asn-Cys-Asn-Asp-Asn-Leu-Asp-Gly-
771 Asn-Cys-Leu-Ile-Cys-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asp-Asn-Leu-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asn-Asp-Asn-Leu-Asp-Cys-
771 Asn-Cys-Asp-Asn-Leu-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asp-Asn-Leu-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asp-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asp-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asp-Asp-Ser-Leu-Ser-Gly-
771 Asn-Cys-Asp-Ser-His-Gly-Thr-Thr-
771 Asn-Ser-Gly-
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1031 Asn-Thr-Gly-Glu-Lys-Cys-Ser-Glu-Cys1041 Let-Pro-Asn-Thr-Trp-Gly-His-Ser-Tle-Val1051 Thr-Gly-Cys-Lys-Nan-Cys-Ser-Thr1061 Val-Gly-Ser-Leu-Ala-Ser-Gln-Cys-Asn-Cys-Ser-Thr1071 Asn-Thr-Cly-Gln-Cys-Ser-Gln-Cys-Asn-Cys-Ser-Thr1091 Arg-Gly-His-Trp-Asn-Tyr-Rro-Leu-Cys-Thr1091 Arg-Gly-His-Trp-Asn-Tyr-Rro-Leu-Cys-Thr1091 Arg-Gly-His-Trp-Asn-Tyr-Rro-Leu-Cys-Thr1191 Ala-Thr-Thr-Cys-Ser-Asp-Leu-Pro-Gly-Thr-Asg1111 Cys-Ser-Gly-Met-Lys-Cys-Phe-Gly-Tys-Phe-Gly1112 Cys-Ser-Gly-Met-Lys-Cys-Phe-Gly-Ys-Phe-Gly1113 Ala-Thr-Thr-Cys-Ser-Asp-Glu-Thr-Gly-Gln-Cys1114 Cys-Asp-Arg-Cys-Phe-Gly-Vs-Phe-Gln-Thr-Ser1115 Leu-Rsp-Ala-Lys-Cys-Phe-Gly-Ys-Phe-Gln-Thr-Ite1116 Trp-Val-Thr-Leu-Ser-Asp-Glu-Gln-Thr-Ite1117 Leu-Rsp-Ala-Lys-Gly-Ile-Ala-Lys-Gln-Thr-Ite1118 Trp-Val-Thr-Lys-Gly-Ile-Ala-Lys-Gln-Thr-Ite1121 Arg-Gln-Glu-Leu-His-Leu-Glu-Gln-Thr-Ite1121 Arg-Gln-Glu-Leu-His-Leu-Glu-Cly-Val1121 Arg-Gln-Glu-Leu-His-Leu-Glu-Cly-Lys1211 Pro-Gly-Phe-Ala-Thr-Tyr-Lys-Pro-Gln-Val1221 Arg-Gln-Glu-Leu-His-Tuy-Hys-Pro-Gln-Val1221 Trp-Lys-Leu-Met-Ala-Tyr-Gly-Jys-Pro-Cln-Val1221 Trp-Lys-Leu-Met-Ala-Tyr-Gly-Jys-Pro-Cln-Val1221 Trp-Lys-Leu-Met-Ala-Thr-Tyr-Lys-Pro-Gln-Val1221 Trp-Lys-Leu-Met-Ala-Thr-Tyr-Lys-Pro-Gln-Val1221 Trp-Cys-Asp-Asp-Phe-Leu-Asp-Glu-Thr1231 Trp-Cys-Asp-Asp-Phe-Leu-Asp-Ile-Leu-Thr1231 Trp-Cys-Ser-Glu-Asp-Phe-Leu-Asp-Ile-Leu-Thr1231 Trp-Cys-Ser-Glu-Asp-Phe-Leu-Asp-Ile-Leu-Thr1231 Trp-Cys-Ser-Glu-Asp-Phe-Cys-Glu-Thr1231 Trp-Cys-Ser-Gly-Phe-Thr-Val1231 Trp-Cys-Ser-Gly-Phe-Thr-Ser-Asp-Cys-Pro-Pro1231 Gly-Asp-Phe-Cys-Glu-Trp-Cys-Asp-Cys-Pro-Pro1231 Gly-Asp-Phe-Cys-Glu-Thr-Cys1231 Trp-Tyr-Gly-Js-Rer-Gly-Ser-Pro-Pro1231 Gly-Asp-Cys-Pro-Thr-Ile1231 Trp-Cys-Cys-Asp-Pro-Gly-Pro-Thr-Ile1231 Trp-Cys-Cys-Asp-Cys-Gly-Pro-Ser-Cys1231 Gly-Asp-Cys-Pro-Thr-Gly-Ser-Pro-Ser-Cys1231 Gly-Asp-Cys-Cys-Asp-Pro-Gly-Pro-Ser-Cys1231 Gly-Asp-Cys-Cys-Asp-Cys-Gly-Tyr-Asp-Cys1231 Gly-Asp-Cys-Pro-Ser-Ser-Pro-Ser-Cys1231 Gly-Asp-Cys-Pro-Ser-Cys1231 Gly-Asp-Cys-Cys-Asp-Cys-Cys-Asp-Cys-

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2171 Lys-Th-Ala-Val-Ala-Asp-Asn-Leu-Leu-Phe-
2181 Tyr-Leu-Gly-Ser-Ala-Lys-Phe-Ile-Asp-Phe-
2181 Tyr-Leu-Gly-Ser-Ala-Lys-Phe-Ile-Asp-Phe-
2191 Leu-Ala-Ile-Glu-Met-Arg-Lys-Gly-Lys-Val-
2201 Ser-Phe-Leu-Trp-Ile-Val-Gly-Ser-Gly-Val-
2201 Ser-Phe-Leu-Trp-Ile-Val-Gly-Ser-Gly-Val-
2211 Gly-Arg-Val-Gly-Phe-Pro-Asp-Leu-Thr-Ile-
2221 Asp-Asp-Ser-Tyr-Trp-Tyr-Arg-Ile-Glu-Ala-
2231 Ser-Arg-Thr-Gly-Yarg-Asn-Gly-Ser-Val-Ser-
2251 Met-Val-Pro-Ser-Thr-Tyr-His-Ser-Val-Ser-
2251 Met-Val-Pro-Ser-Thr-Tyr-Phe-Val-Gly-Gly-Leu-
2261 Pro-Pro-Gly-Tyr-Thr-Ile-Leu-Asp-Val-Asp-
2271 Ala-Asn-Ala-Met-Leu-Phe-Val-Gly-Gly-Leu-
2281 Thr-Gly-Lys-Ile-Lys-Lys-Pro-Ile-Gly-
2291 Arg-Val-Ile-Thr-Phe-Thr-Gly-Cys-Met-Gly-
2291 Arg-Val-Ile-Thr-Phe-Thr-Gly-Cys-Met-Gly-
2391 Leu-Trp-Asp-Phe-Asp-Asn-Lys-Pro-Ile-Gly-
2391 Glu-Thr-Tyr-Phe-Asp-Clu-Lys-Glu-Gly-Asp-
2391 Glu-Trp-Asp-Phe-Asp-Asp-Leu-Val-Ser-Arg-Pro-
2391 Glu-Trp-Asp-Phe-Arg-Clu-Lys-Glu-Gly-Pro-
2391 Glu-Trp-Asp-Phe-Arg-Thr-Ile-Ser-Thr-Val-
2391 Glu-Asp-Thr-Tyr-Phe-Tyr-Dhe-Ser-Ser-Ser-
2391 Glu-Asp-His-Val-Lys-Clu-Lys-Glu-Leu-Ser-
2391 Asp-Gly-His-Val-Lys-Val-Ser-Arg-Leu-
2391 Asp-Gly-His-Val-Lys-Clu-Ala-Thr-Arg-Asp-
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2401 Gly-Ser-Gly-Met-Thr-Ser-Val-Val-Ser-An-
2401 Gly-Ser-Gly-Met-Thr-Ser-Val-Val-Ser-An-
2401 Gly-Ser-Gly-Met-Thr-Ser-Val-Val-Ser-An-
2401 Gly-Ser-Gly-Met-Thr-Ser-Val-Val-Ser-An-
2401 Gly-Ser-Gly-Met-Thr-Ser-Val-Val-Ser-An-
2401 Gly-Ser-Gly-Leu-Asp-Ile-Gln-Lys-Gln-Ala-
241 Gln-Glu-Glu-Asn-Val-Asp-Ile-Gln-Lys-Gln-Ala-
2461 Asp-Asp-Lys-Ile-Tyr-Phe-Gly-Leu-Lys-Ala-
2461 Asp-Asp-Lys-Ile-Tyr-Phe-Gly-Leu-Lys-Ala-
2461 Asp-Asp-Lys-Ile-Tyr-Phe-Gly-Leu-Lys-Ala-
2461 Asp-Asp-Lys-Ile-Tyr-Phe-Gly-Leu-Lys-Ala-
2461 Asp-Asp-Lys-Ile-Gly-Lys-Cly-Leu-
2461 Asp-Asp-Lys-Ile-Gly-Lys-Cly-Leu-
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2461 Asp-Asp-Lys-Ile-Gly-Gly-Leu-
2461 Asp-Asp-Lys-Ile-Gly-Gly-Leu-
2461 Asp-Asp-Lys-Ile-Gly-Gly-Gly-Leu-
2461 Asp-Asp-Lys-Ile-Gly-Gly-
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1041 Ser-Thr-Val-Gly-Ser-Leu-Asp-Phe-Gln-Cys-
1051 Zen-Wal-Asn-Thr-Gly-Gln-Cys-Asn-Cys-His-
1061 Cys-Ser-Arg-Gly-His-Trp-Asn-Cyr-Pro-Arg-
1071 Cys-Ser-Arg-Gly-His-Trp-Asn-Cyr-Pro-Arg-
1071 Cys-Ser-Arg-Gly-His-Trp-Asn-Cyr-Pro-Arg-
1071 Lys-Lys-Cys-Ser-Cys-Ser-App-Gln-Thr-Gly-
1171 Ill-His-Cys-App-Cys-Pro-Cys-Pro-Gly-Fro-
1171 Thr-Gly-Leu-App-Ala-Thr-Thr-Cys-App-Gln-Thr-Gly-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Aan-Pro-Leu-Gly-
1181 Gln-His-Cys-Ser-Gly-Ala-Lys-Aan-Pro-Leu-Gly-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Aan-Pro-Leu-Gly-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Ala-Glu-Ala-Leu-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Ala-Glu-Ala-Leu-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Ala-Glu-Ala-Pro-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Gly-The-Pro-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Ala-Glu-Ala-Pro-
1171 Thr-Gln-Cys-Ser-Gly-Ala-Lys-Gly-Gly-Lys-
1170 Leu-Net-Arg-Glu-App-Leu-His-Met-Asp-
1171 Thr-Gly-Sp-Leu-Pro-Glu-Gln-Pro-
1171 Thr-Gly-Sp-Leu-Pro-Gly-Gly-Gly-Lys-
1171 Thr-Gly-Sp-Leu-Het-Ala-Tyr-Gly-Gly-Lys-
1171 Thr-Ser-Glu-Met-Thr-Lys-Glu-Trp-Lys-
1171 Thr-Ala-Arg-Ill-Fle-Gly-Gln-Leu-His-Met-Arg-
1171 Ala-Pro-Leu-His-Het-Arg-Glu-App-Pro-Thr-
1271 Ala-Pro-Leu-His-Het-Thr-Gly-Asp-Pro-Arg-His-
1271 Ala-Pro-Leu-His-Ser-Met-Arg-His-Met-Ala-
1271 Ala-Pro-Leu-Hy-Asp-Ile-His-Met-Arg-
1371 Ala-Pro-Leu-Hy-Asp-Pro-Arg-Val-His-Het-
1371 Ala-Pro-Leu-Hy-Asp-Pro-Cys-Glu-Trp-Cys-Glu-Arg-
1371 Ala-Cys-Pro-Gly-Ang-Pro-Cys-Glu-Arg-
1371 Ala-Cys-Pro-Gly-Ang-Pro-Cys-Glu-Arg-
1371 Ala-Cys-Pro-Gly-Phe-Tyr-Arg-Leu-Arg-
1371 Ala-Cys-Pro-Gly-Phe-Tyr-Arg-Lys-Pro-Gly-
1371 Thr-Gly-Asp-Pro-Cys-Glu-Ang-Pys-Cys-Ala-
1371 Ala-Cys-Pro-Cys-Glu-Arg-Cys-Ala-
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1371 Ala-Cys-Pro-Cys-Glu-Ang-Cys-App-Pro-Gly-
1371 Thr-Gly-Asp-Leu-Pro-Cys-Ang-Pro-Gly-
1371 Thr-Gly-Asp-Leu-Pro-Cys-Ang-Pro-Gly-
1371 Thr-Gly-Asp-Leu-Pro-Cys-Ang-Pro-Cys-Ala-
1371 Thr-Gly-Asp-Leu-Pro-Cys-Ang-Pro-Gly-
1371 Thr-Gly-Asp-Leu-Pro-Cys-Ang-Pro-Gly-
1371 Thr-Gly-Asp-Leu-Pro-Gly-Asp-Pro-Gly-
1371 Thr-Gly-Asp-Cys-Thr-Arg-Glu-Gly-
1371 Thr-Gly-Asp-P
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1611 Ille-Gin-Leu-Ala-Giu-Giy-Asn-Leu-Asn-Thr-
1621 Leu-Val-Thr-Glu-Metr Asn-Giu-Leu-Leu-Thr-
1631 Arg-Ala-Thr-Glu-Metr Asn-Giu-Leu-Leu-Thr-
1641 Gin-Th-Giy-Gin-Asp-Ala-Giu-Arg-Thr-Asn-
1651 Thr-Arg-Ala-Lys-Ser-Leu-Giy-Giu-Phe-Ile-
1661 Lys-Giu-Leu-Ala-Arg-Asp-Ala-Giu-Ala-Val-
1671 Asn-Giu-Lys-Ala-Ile-Lys-Giu-Ile-Asp-
1691 Asn-Giu-Lys-Ala-Ile-Lys-Giu-Ile-Asp-
1791 Gin-Met-Ile-Lys-Gil-Ile-La-Arg-Asp-Giu-Ala-Giu-Ala-
1791 Lau-Giu-Giy-Giu-Giy-Leu-Gin-Lys-Giu-Ile-Asp-
1791 Lau-Giu-Sys-Giu-Ile-Asp-Giu-Ile-Asp-
1791 Lau-Giu-Sys-Giu-Ile-Asp-Tyr-Lys-Asn-
1791 Lau-Giu-Sys-Giu-Giu-Bet-Giu-Lys-Giu-
1791 Ala-Thr-Asp-Lys-Lys-Leu-Phe-Giu-Ala-Ser-Arg-
1791 Lau-Giu-Giy-Asn-Asp-Ile-Leu-Leu-Lys-
1791 Lau-Giu-Giu-Sys-Giu-Ile-Asp-Tyr-Lys-Asn-Met-Thr-
1791 Lau-Giu-Giy-Asn-Asp-Ile-Leu-Leu-Asp-Giu-
1891 Lys-Giu-Giy-Asn-Asp-Ile-Leu-Leu-Asp-Asp-
1892 Leu-Phe-Ala-Val-Asn-Gin-Lys-Asn-Met-Thr-
1893 Ile-Asp-Asp-Tyr-Asp-Lau-Sp-Giu-Ala-Asn-Asp-
1894 Leu-Phe-Ala-Val-Asn-Asp-Ile-Leu-Asp-Asp-
1895 Lys-Ile-Asp-Asp-Tile-Asp-Ile-Giu-Asn-Asp-
1896 Lys-Giu-Ser-His-Ala-Asp-Giu-Ile-Asp-Asp-
1897 Asn-Arg-Lys-Leu-Ala-Giu-Lys-Val-Asn-Asp-
1898 Iser-Ser-Ala-Val-Leu-Asp-Giy-Ile-Leu-Asp-Asp-
1991 Lau-Asp-Arg-Lys-Leu-Ala-Giu-Lys-Val-Ash-Ala-
1991 Lys-Giu-Ala-Lys-Asp-Ile-Giu-Leu-Asp-Giy-Ile-
1991 Lys-Giu-Ala-Lys-Asp-Ile-Giu-Ala-Asp-
1991 Lys-Giu-Ala-Phe-Lys-Asp-Leu-Asp-Giy-Ile-Leu-Asp-
1991 Lys-Giu-Ala-Asp-Ala-Tyr-Ser-Asn-Ile-Lys-
1991 Lys-Giu-Ala-Asp-Ala-Tyr-Ser-Asn-Ile-Lys-
1991 Lys-Giu-Ala-Asp-Giu-Ala-Asp-Giu-Ala-Asp-
1991 Lys-Giu-Ala-Asp-Ala-Tyr-Ser-Asn-Ile-Lys-
1991 Lys-Giu-Ala-Asp-Ala-Tyr-Sep-Ile-Giu-Ala-
1991 Lys-Giu-Ala-Asp-Ala-Tyr-Sep-Ile-
1991 Lys-Giu-Ala-Asp-Ala-Tyr-Sep-Ile-
1991 Lys-Giu-Ala-Asp-Ala-Tyr-Asp-Ile-
2001 Lys-Leu-Ala-Asp-Ala-Tyr-Asp-Ile-
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2001 Lys-Leu-Giy-Asp-Ala-Lys-Giy-Cys-Leu-Giy-Giy-Leu-
2001 Ala-Asp-Asp-Ala-Tyr-Asp-Tyr-Asp-Ly-
2001 Lys-Leu-Giy-Sep-Ala-Tyr-Asp-Ly-
2001 Lys-Lys-Sp-Ile-Asp-Ala-Lys-Sp-Ile-
2001 Lys-Lys-Sp-Il
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191 Gly-Val-Gly-Arg-Val-Glu-Tyr-Pro-Asp-Leu-
201 Thr-11e-Asp-Asp-Ser-Tyr-Trp-Tyr-Arg-Ileu-
201 Thr-11e-Asp-Asp-Ser-Tyr-Trp-Tyr-Arg-Ileu-
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201 Thr-12e-Asp-Asp-Ser-Tyr-Trp-Tyr-Arg-Ileu-
201 Thr-Ser-Val-Arg-Ala-Leu-Asp-Gly-Pro-Lys-
211 La-Ser-11e-Val-Pro-Ser-Thr-His-His-Ser-
221 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-His-Leu-Asp-
221 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-His-Leu-Asp-
221 Thr-Ser-Pro-Pro-Pro-Phe-Arg-Glu-Lys-Gly-
221 Thr-Val-Asp-Ala-Asp-Nen-Pro-Phe-Arg-Glu-Lys-Glu-
221 Thr-Val-Ser-Pro-
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221 Thr-Val-Ser-Oly-Tyr-Pro-Asp-Ile-Ser-
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241 Lys-Ala-Asp-Sep-Cly-Ser-Ser-Met-Lys-
242 Met-Ser-Ser-Met-Lys-Met-Lys-Tyr-
243 Asp-Leu-Gly-Ser-Sep-Leu-Lys-Tyr-
244 Lys-Ala-Asp-Cly-Val-Asp-Leu-Lys-Tyr-
245 Ala-Asp-Ser-Sep-Clu-Val-Asp-Leu-Lys-Tyr-
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551 Leu-Gly-Asm-Lys-Leu-Pro-Ala-Pro-Tyr-
652 Ich-Ise-Gly-Glu-Glu-Glu-Glu-Asp-Thr-11e-Ser-Tyr-Asp-Leu-
651 Glu-Glu-Glu-Glu-Glu-Asp-Thr-11e-Ser-Tyr-Asp-Leu-
651 Asp-Leu-Ser-Ila-Glu-Asp-Thr-Glu-Arg-Val-
651 Asp-Leu-Ser-Ila-Glu-Asp-Thr-Glu-Arg-Val-
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651 Asp-Leu-Ser-Ila-Ser-Thr-Ala-Glu-Asp-Glu-
651 Asp-Leu-Ser-Ila-Ser-Thr-Ala-Glu-Asp-Glu-
652 Ser-Phe-Gly-Met-Asp-Ala-Ila-Phe-Arg-Leu-
653 Intr-Gly-Ser-Ser-Cys-Glu-Ser-Cys-Trp-
654 Ser-Ser-Val-Asn-Leu-Glu-Ser-Ila-Ala-Ala-
655 Asn-Val-Asp-Glu-Phe-Met-Thr-Val-Cys-Glu-Ser-Cys-Trp-
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4 <u>1</u> -n	Ile-Lys-Asp-Tyr-Ile-Asp-Glu-Ala-G	1931
r-As	a-Thr-Ala-Ala-Phe-Lys-Ala-Tyr-S	1921
y-lle-	A5n-Asp-Ser-Ser-Ala-Vai-Leu-Asp-G	1911
Ō	Ser-Gln-Ala-Glu-Ser-His-Ala-Ala-	1891
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n-61u-	1 Asn-Asp-Lys-Ile-Asp-Asp-Leu-Ser-Gl	1871
e-Gln-	er-Ile-Ile-Asp-Tyr-Val-Glu-Asp-I	1851
As	u-Ala-Asn-Arg-Leu-Ala-Asp-Glu-I	1841
u-Asn-	-Asn-Asp-	1831
<u>.</u> 2	t-Thr-Ala-Leu-Glu-Lys-Lys-Lys-G	1811
s-Asn-	Asn-Arg-Leu-Phe-Ala-Val-Asn-Gln-	1801
Ž!	g-Glu-Ala-Thr-Asp-Lys-Ile-	1791
r-Lys-	u-Arg-Glu-Lys-Leu-Ala-Asp-T s-Val-Asp-Psp-Ala-Trp-Asp-T	1771
5	r-Arg-Gly-Glu-Asn-Glu-Glu-Met-G	1761
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Ile-Gln-Phe-Asp-Gly-Glu-Gly-Tyr-Ala-Leu-
Val-Ser-Arg-Pro-Ile-Arg-Tyr-Pro-Asn-
Ile-Ser-Thr-Val-Met-Phe-Lys-Phe-Arg-Thr-
Gln-Arg-Pro-Gln-Gln-Gln-Arg-Gln-Ser-Gln-Ala-His-Gln-Gln-Arg-Gly-Leu-Phe-Pro-Ala-Val-Leu-Ann-Leu-Ala-Ser-Asn-Ala-Leu-Ile-Thr-Thr-Asn-Ala-Thr-Cys-Gly-Glu-Lys-Gly-Pro-Glu-Met-Tyr-Cys-Lys-Leu-Val-Glu-His-
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222 Leu-Arg-Phe-Chr-Ser-Ala-Arg Tyr-IIe-Arg-
222 Leu-Arg-Phe-Gln-Arg-IIe-Arg-Thr-Lou-Asn-
223 Ala-Asp-Leu-Met-Wet-Phe-Ala-His-Lys-Asp-
224 Pro-Arg-Glu-IIe-Asp-Pro-IIe-Val-Thr-Arg-
225 Arg-Tyr-Tyr-Tyr-Ser-Val-Lys-Asp-IIe-Ser-
226 Arg-Tyr-Tyr-Tyr-Ser-Val-Lys-Asp-IIe-Ser-
227 Ala-Arg-Ala-Cys-Pro-Leu-Asp-Pro-Ala-Thr-
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228 Asn-Lys-Ser-Arg-Cys-Glu-Cys-Glu-His-Asn-
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232 Val-Ser-Leu-Asn-Tyr-Pro-Arg-Pro-Cys-Gln-
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141 Tyr-Pro-Asp-Cys-Lys-Ala-Cys-Asn-Cys-Ser-
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171 Glu-Gly-Gly-Asp-Cys-Ser-Arg-Cys-Lys-Ser-
171 Glu-Gly-Asp-Leu-Gln-Glu-Asp-Asn-Trp-
181 Gly-Phe-Phe-Asn-Leu-Gln-Glu-Asp-Asn-Trp-
191 Lys-Gly-Cys-Asp-Glu-Cys-Phe-Cys-Ser-Gly-
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195 Cys-Sep-Glu-Cys-Phe-Cys-Ser-
195 Cys-Sep-Glu-Cys-Phe-Cys-Sep-Glu-Cys-Phe-Cys-Sep-Glu-Cys-Phe-Cys-Sep-Glu-Cys-Phe-Cys-Sep-Glu-Cys-Phe-Cys-Sep-Glu-Cys-Phe-Cys-Sep-Cys-
195 Cys-Sep-Glu-Cys-Phe-Cys-Sep-Cys-Phe-Cys-Sep-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-Phe-Cys-
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Tyr-Pro-Arg-Thr-Gly-Pro-Pro-Ser-Tyr-Ala-
Lys-Asp-Asp-Glu-Val-Ile-Cys-Thr-Ser-Phe-
Tyr-Ser-Lys-1le-His-Pro-Leu-Glu-Asn-Gly-Arg-
Glu-Ile-His-Ile-Ser-Leu-Ile-Asn-Gly-Arg-
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Tyr-Val-Thr-Ile-Thr-Leu-Asp-Leu-Gln-Gln-
Val-Phe-Gln-Ile-Ala-Tyr-Val-Ile-Val-Lys-
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Pro-Asn-Gln-Arg-His-Pro-Ile-Thr-Asn-Ala-
Ile-Asp-Gly-Lys-Asn-Thr-Trp-Trp-Gln-Ser-
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Ala-Arg-Arg-Gly-Leu-Ala-Pro-Gly-Ser-Cys-
His-Cys-Lys-Thr-Gly-Phe-Gly-Gly-Val-Ser-
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Ile-Leu-Glu-Arg-Ser-Leu-Asp-Asp-Val-Glu-
Asn-Lys-Leu-Pro-Ala-Val-Gly-Gly-Gln-Leu-
Thr-Phe-Thr-Ile-Ser-Tyr-Asp-Leu-Glu-Glu-
Glu-Glu-Glu-Asp-Thr-Glu-Arg-Val-Leu-Gln-
                                                                                                                                                                                   Trp-Tyr-Leu-Thr-Asp-Leu-Pro-Gly-Arg-Ile-Arg-Val-Ala-Pro-Gln-Gln-Asp-Asp-Leu-Asp-Ser-Pro-Gln-Gln-B-Ser-Tle-Ser-Asp-Ala-Glu-Ala-Arg-Gln-Ala-Leu-Pro-His-Ser-Tyr-Glu-Ala-Arg-Gln-Ala-Leu-Pro-His-Ser-Tyr-
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                                                                                                                                          Tyr-Trp-Ser-Ala-Pro-Ala-Pro-Tyr-Leu-Gly-
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g-Thr-Trp-Val-Thr-Leu-Lys-Ala-Glu-G	Ġ	1161
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Cys-Ser-Ser-Cys-Tyr-Cys-Phe-Gly-Thr-Thr-	S 2	1141
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ys-Thr-Cys-Lys-Val-Asn-Val-Glu-Gl	2 (- 0
r-Asp-Ala-Thr-Thr-Cys-Asp-Ser-Glu-	1 7	
s-Asn-Leu-Cys-Asp-Cys-Phe-Leu-Pro-Gl	Qs-	1081
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-Thr-Gly-Arg-Tyr-Cys-Glu-Leu-Cys-Al		- 7
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p-Gly-Cys-Pro-Val-Gly-Tyr-Thr-Gly-	י קר	H
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1741 Gly-Glu-Asn-Glu-Glu-Met-Glu-Lys-Asp-Leu-
1751 kal-Asp-Cy-Lou-Ala-Asp-Cy-Lys-Asn-Lys-
1761 val-Asp-Lys-Lou-Ala-Asp-Cyr-Lys-Asn-Lys-
1761 la-Cher-Asp-Lys-Ile-Asp-Clu-Ala-Asp-Cyr-
1761 Leu-Phe-Ala-Val-Asn-Gln-Lys-Asn-Met-Thr-
1861 Lys-Glu-Gly-Asn-Asp-Ile-Clu-Ala-Val-Clu-
1861 Lys-Glu-Gly-Asn-Asp-Ile-Clu-Ala-Val-Clu-
1861 Lys-Ile-Asp-Asp-Lys-Lys-Lys-Glu-Ala-Val-Clu-
1861 Lys-Ile-Asp-Asp-Lys-Leu-Asp-Glu-Ile-Cu-Asp-Glu-
1861 Lys-Ile-Asp-Asp-Leu-Ser-Glu-Glu-Ile-Asp-Asp-
1861 Lys-Ile-Asp-Asp-Leu-Asp-Glu-Ile-Clu-Asp-
1861 Lys-Ile-Asp-Asp-Leu-Asp-Glu-Ile-Clu-Asp-
1861 Lys-Ile-Asp-Asp-Leu-Asp-Glu-Ile-Clu-Asp-
1861 Lys-Ile-Asp-Asp-Leu-Asp-Glu-Ile-Clu-Asp-
1861 Lys-Ile-Asp-Asp-Leu-Asp-Glu-Ile-Ser-Gln-
1861 Asp-Arg-Lys-Asn-Ile-Ser-Gln-Glu-Lys-Val-Ala-
1861 Lys-Ile-Asp-Asp-Leu-Asp-Glu-Lys-Val-Ala-
1861 Lys-Glu-Ala-Val-Leu-Asp-Glu-Lys-Val-Ala-
1861 Lys-Glu-Ala-Val-Asp-Ile-Ser-Hys-Asn-Ile-Ile-
1861 Lys-Glu-Ala-Lys-Asp-Ile-Glu-Lys-Val-Ala-
1861 Lys-Glu-Ala-Lys-Asp-Ile-Ile-Ilys-Glu-Lys-Val-Ala-
1861 Lys-Glu-Ala-Lys-Asp-Leu-Lys-Ile-Ile-
1861 Lys-Glu-Ala-Asp-Ala-Lys-Asp-Ile-Ile-Ilys-Glu-Lys-Leu-
1861 Lys-Glu-Ala-Asp-Ala-Lys-Asp-Ile-Ilys-Glu-Lys-Leu-
1861 Lys-Ser-Phe-Arg-Ile-Ile-Ilys-Glu-Lys-Leu-
1861 Lys-Ser-Phe-Arg-Ile-Ile-Ilys-Glu-Ala-Lys-
1861 Lys-Leu-Ala-Asp-Ala-Lys-Asp-Ile-Ile-
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1861 Lys-Lys-Asp-Ill-Ala-Lys-Asp-Ill-Ile-Asp-Lys-
1861 Leu-Lys-Lys-Asp-Ill-Ala-Lys-Asp-Ill-Ile-Asp-Lys-
1861 Leu-Lys-Lys-Asp-Ill-Ala-Lys-Asp-Ill-Ile-Asp-Lys-
1861 La-Asp-Asp-Ill-Ala-Lys-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala-Asp-Asp-Ill-Ala
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206A; 157R; 163N; 163D; 0 B; 16.
246L; 186K; 46 M; 104F; 172P; 19:
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AAB19791 Protein
DGENE
Purified laminin 2 protein, useful for research and therapeutic purposes
including peripheral nerve regeneration, treatment of degenerative muscle
disorders, anglogenesis regulation, and ex vivo cell therapy -
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1 Met-Pro-Gly-Ala-Ala-Gly-Val-Leu-Leu-Leu-
1 Leu-Ser-Gly-Gly-Leu-Gly-Val-
21 Gln-Ala-Gln-Arg-Fro-Gln-Gln-Arg-Gly-Val-
21 Gln-Ala-Gln-Arg-Fro-Gln-Gln-Arg-Gly-Leu-Phe-
41 Ser-Gln-Ala-His-Gln-Gln-Arg-Gly-Leu-Phe-
42 Pro-Ala-Val-Leu-Asn-Leu-Ala-Ser-Asn-Ala-
43 Leu-Lie-Fhr-Thr-Asn-Ala-Thr-Cys-Gly-Glu-
46 Lys-Gly-Pro-Glu-Met-Tyr-Cys-Lys-Leu-Val-
47 Lys-Gly-Pro-Glu-Met-Tyr-Cys-Lys-Leu-Val-
48 Pro-Gln-Cys-Arg-Tle-Cys-Asn-Gln-Arg-Asn-Ser-Fro-
49 Pro-Gln-Cys-Arg-Tle-Cys-Asn-Gln-Arg-His-Pro-Tle-Thr-
40 Lys-Gly-Pro-Asn-Gln-Arg-His-Pro-Tle-Thr-
41 Lys-Gly-Pro-Sen-Tle-Lys-Asn-Gly-Tle-Glu-
41 Lys-Gly-Pro-Sen-Tle-Lys-Asn-Gly-Tle-Glu-
41 Lys-Gly-Pro-Sen-Tle-Thr-Leu-Asp-Leu-
41 Lys-Gly-Pro-Sen-Thr-Tle-Thr-Leu-Asp-Leu-
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221 Phe-Asp-Gly-Glu-Gly-Tyr-Ala Leu-Val-Ser-
321 Arg-Pro-Ile-Arg-Tyr-Tyr-Pro-Asn-Ile-Ser-
321 Thr-Val-Met-Phe-Lys-Phe-Arg-Thr-Phe-Ser-
321 Thr-Val-Met-Phe-Lys-Phe-Arg-Thr-Phe-Ser-
321 Inr-Val-Met-Phe-Lys-Phe-Met-Ser-Val-Glu-
321 Leu-Thr-Asp-Gly-His-Ile-Lys-Val-Ser-Tyr-
321 Leu-Thr-Asp-Gly-His-Ile-Lys-Val-Ser-Tyr-
321 Leu-Thr-Asp-Gly-His-Ile-Lys-Val-Ser-Tyr-
322 Leu-Thr-Asp-Gly-His-Ile-Lys-Val-Ser-Tyr-
423 Ser-Asn-Gln-Asn-His-Asn-Asp-Gly-Lys-Trp-
424 Thr-Asn-Gln-Glu-Asn-Ile-Ala-Thr-Asp-
425 Thr-Asn-Gly-Asn-Asn-Phe-Gly-Leu-Asp-Leu-
426 Leu-Pro-Thr-Leu-Asp-Lys-Ile-Gly-Gly-
427 Thr-Asn-Asp-Lys-Ile-Tyr-Phe-Gly-Gly-
428 Lys-Ala-Asp-Lse-Asp-Lys-Tyr-Phe-Gly-Gly-
429 Lys-Ala-Asp-Lse-Asp-Lu-Lys-
421 Lys-Ala-Asp-Lse-Asp-Lu-Lys-
421 Lys-Ala-Asp-Clu-Val-Asn-Leu-Lys-Lys-Tyr-
422 Thr-Asn-Pro-Glu-Val-Asn-Leu-Lys-Lys-Tyr-
423 Lau-Pro-Thr-Leu-Val-Asn-Leu-Lys-Lys-Tyr-
424 Lys-Ala-Asp-Pro-Glu-Val-Asn-Leu-Lys-Lys-Tyr-
425 Lse-Pro-Glu-Val-Asn-Leu-Lys-Lys-Tyr-
426 Ala-Asp-Pro-Glu-Val-Asn-Leu-Lys-Lys-
427 Lys-Tyr-
428 Lys-Met-Lys-
429 Lys-Tyr-
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421 Lys-Ala-Syp-Clu-Val-Asn-Leu-Lys-
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6 Y; 157V;
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721 Tyr-Pro-Thr-Asp-Gly-Ser-Ile-Ala-Ala-Ala-Ala-Y22 Val-Glu-Val-Cys-Glu-Cys-Pro-Pro-Gly-Tyr-731 Thr-Gly-Ser-Ser-Cys-Glu-Ser-Cys-Tp-Pro-741 Arg-His-Arg-Arg-Val-Asn-Gly-Thr-Ile-Phe-751 Gly-Glu-Cys-Glu-Cys-Glu-Pro-Cys-Glu-Pro-771 Gly-His-Ala-Glu-Gro-Ser-Asp-Asp-Val-Thr-771 Gly-Glu-Cys-Leu-Asn-Cys-Lys-Asp-His-Thr-771 Gly-Glu-Cys-Leu-Asn-Cys-Lys-Asp-His-Thr-781 Gly-Glu-Cys-Leu-Asn-Cys-Asp-Cys-Glu-Pro-79-Gly-Fro-Tyr-Gly-Glu-Pro-Tyr-Gly-Glu-Pro-Tyr-Gly-Glu-Pro-Tyr-Gly-Glu-Pro-Tyr-Gly-Glu-Pro-Ys-Asp-Asp-Asn-Asp-Asn-His-Cys-Asp-Cys-Ala-Clu-Cly-Ser-Cys-Asp-Cys-Ala-Clu-Cly-Ser-Cys-Asp-Cys-Ala-Clu-Cly-Ser-Cys-Asp-Asp-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Asp-Asn-Sp-Cys-Glu-Pro-Cys-Glu-Cys-Asn-Cys-Asn-Sp-Cys-Asn-Asp-Asn-Sp-Cys-Asn-Asp-Asn-Sp-Cys-Clu-Leu-Sp-Cys-Asn-Asp-Asn-Sp-Cys-Asn-Cys-Glu-Cys-Asn-Cys-Asn-Sp-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Sp-Chu-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-Asn-Cys-A
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É	In-XIa-Yall-XId-Hen-YIa-Yal-AId-	
	hr-Leu-Lys-Glu-Gly-Asn-Asp-Ile-Le	1831
Kn-	Met-Thr-Ala-beu-Glu-bys-bys-bys-Glu-J Val-Glu-Ser-Gly-Lys-Arg-Gln-Ile-Glu-J	1821
	n-Arg-Leu-Phe-Ala-Val-Asn-Gln-Lys-	
Ala-	g-Glu-Ala-Thr-Asp-Lys-Ile-Arg-Glu-	
Teu-	n-Lys-Val-Asp-Asp-Ala-Trp-Asp-Leu-	1781
, 1 1 1 1	-I.eArg-Gly-Glu-Asn-Glu-Glu-Met-Glu- -Arg-Gly-Glu-Asn-Glu-Glu-Met-Glu-	
Glu-	u-Lys-Lys-Val-Lys-Lys-Leu-Phe-Gly-	1751
	:-Asp-Glu-Leu-Val-Ala-Ala-Glu-Ala-	1741
Arg- Ala-	vs-Asp-Gin-Met-lie-Lys-Giu-Leu-Arg-	1721
Glu-	u-Arg-Asn-Leu-Glu-Gly-Leu-Gln-Lys-	1711
he-	lu-Thr-Leu-Gly-Thr-Arg-Asp-Glu-Ala-	1701
Asn-	la-Val-Asn-Glu-Lys-Ala-Ile-Lys-Leu-	1691
61u-	-Kan-Thr-Arg-Ala-bla-Arg-Asp-Ala- -Kile-Lvs-Glu-Leu-Ala-Arg-Asp-Ala-	1681
Arg-	ly-Glu-Gln-Thr-Gly-Gln-Asp-Ala-Glu-	1661
Asp-	eu-Thr-Arg-Ala-Thr-Lys-Val-Thr-Ala-	1651
Leu-	Leu-Val-Thr-Glu-Met-Asn-Glu-	1641
Ten-	s-Leu-Leu-Ser-Pro-Gin-Arg-Aia-Pro- s-Leu-Leu-Ser-Pro-Gin-Arg-Aia-Pro-	1207
Lys-	-Leu-Glu-Asn-Met-Thr-Gln-Glu-Leu-	1611
yr-	o-Leu-Pro-Ala-Pro-Tyr-Lys-Met-Leu-	1601
Gly-	-Met-Val-Met-Ser-Ile-Asn-Leu-Thr-	1591
Glu-	Gly-Asp-Leu-Ala-Arg-Leu-	1581
	-His-Trp-His-Ala-Arg-Glu-Gly-Trp-	1561
уз-	y-Ala-Thr-Gly-Arg-Lys-Cys-Asp-Gly-	1551
Pro-	ro-Val-Thr-Gly-Phe-Cys-Thr-Cys-Arg-	1541
Asp-	o-Tyr-Gly-Ser-Leu-Pro-Val-Pro-Cys-	1531
n H	o-G1y-Tyr-Thr-G1y-Ser-Pro-G1y-Asn- o-G1y-Tyr-Thr-G1y-Ser-Pro-G1y-Asn-	1511
Ala-	r-Glu-Gly-Gln-Tyr-Cys-Glu-Arg-Cys-	1501
GLy-	p-Tyr-Arg-Cys-Thr-Ala-Cys-Pro-Arg-	1491
n :	r-Pro-Ser-(Vs-Va)-A)a-G)u-G)v-Teu- 8-Pro-Ser-(Vs-Va)-A)a-G)u-G)v-Teu-	1481
i i a -	y-Leu-Pro-Asn-Asp-Cys-Gln-Gln-Cys-	1461
Lys-	-Ala-Leu-Gly-Tyr-Tyr-Gly-Ile-Val-	1451
rq-	s-His-Thr-Ala-Glv-Asp-Phe-Cvs-Glu-	1441
Asp-	n-Cys-Asn-Gly-His-Ser-Ser-Leu-Cys-	1421
Cys-	-Pro-Thr-Leu-Gly-Thr-Cys-Val-Pro-	1411
H I	u-Arg-Ser-Gln-Pro-Gly-Gly-Arg-Thr-	1401
rg-	g-Cys-rio-med-Giy-lpi-sei-Giy-Phe-Tyr-	1391
Cys -	r-Pro-Pro-Ala-Asp-Leu-Ile-Glu-Lys- r-Pro-Pro-Ien-Gly-Tyr-ser-Gly-Leu-	1371
Met-	al-Ala-Glu-Gln-Gly-Arg-Gly-Thr-Thr-	1361
GLu-	-Ser-Arg-Ile-Ser-Glu-Ile-Ser-Met-	1351
Arg-	le-Lys-Ala-Thr-Tyr-Gly-Asn-Phe-Met-	1341
Leu-	s-Arg-Thr-Val-Thr-Arg-Glu-Asp-Phe- b-Ile-Leu-Tvr-Asp-Ile-His-Tvr-Ile-	1321
/al-	rp-Lys-Tyr-Gly-Asp-Asp-Pro-Arg-	1311
F :	g-His-Glu-Ile-Glu-Met-Thr-Glu-Lys-	1301
hr-	-Ala-Ala-Pro-Leu-Ile-Gly-Gln-Leu	1291

1281 Pro-Thr-His-Ala-Arg-Ile-Ile-Val-Arg-His-

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Lys-Glu-Leu-Ile-Asn-Gln-Ala-Arg-Lys-Gln-Ala-Asn-Ser-Ile-Lys-Val-Ser-Val-Ser-Ser-Gly-Gly-Asp-Cys-Ile-Lys-Arg-Thr-Tyr-Lys-Pro-Glu-Ile-Lys-Lys-Gly-Ser-Tyr-Asn-Asn-Ile-Val-Val-Asn-Val-Lys-Thr-Ala-Val-Ala-Asp-Val-Val-Asn-Val-Asn-Val-Lys-Thr-Ala-Val-Ala-Asp-
Val-Glu-Lou-Thr-Asp-Gly-His-Ile-Lys-Val-
Ser-Tyr-Asp-Lou-Gly-Ser-Gly-Met-Ala-Ser-
Val-Val-Ser-Asn-Gln-Asn-His-Asn-Asp-Gly-
                                                                                                                                                         Ser-Pro-Gln-Val-Glu-Asp-Ser-Glu-Gly-Thr-
Ile-Gln-Phe-Asp-Gly-Glu-Gly-Tyr-Rila-Leu-
Val-Ser-Arg-Pro-Ile-Arg-Tryr-Pro-Asn-
Ile-Ser-Arg-Pro-Ile-Arg-Try-Phe-Arg-Thr-
Phe-Ser-Ser-Ser-Ala-Leu-Leu-Met-Tyr-Leu-
                                                                                                                                                                                                                                                                                                                                                                   Gly-Cys-Met-Gly-Glu-Thr-Tyr-Phe-Asp-Asn-Lys-Pro-Ile-Gly-Leu-Trp-Asn-Phe-Arg-Glu-Lys-Gly-Asp-Cys-Lys-Gly-Cys-Thr-Val-
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Gly-Ser-Gly-Val-Gly-Arg-Val-Glu-Tyr-Pro-
Asp-Leu-Thr-Ile-Asp-Asp-Ser-Tyr-Trp-Tyr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Val-Leu-Ala-Gln-Ile-Thr-Glu-Leu-His-Gln-
Asn-Leu-Asp-Gly-Leu-Lys-Lys-Asn-Tyr-Asn-
Lys-Leu-Ala-Asp-Ser-Val-Ala-Lys-Thr-Asn-
Ala-Val-Val-Lys-Asp-Pro-Ser-Lys-Asn-Lys-
Ile-Ile-Ala-Asp-Ala-Asp-Ala-Thr Val-Lys-
Asn-Leu-Glu-Gln-Glu-Ala-Asp-Arg-Leu-Ile-
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Asp-Leu-Leu-Asn-Asp-Thr-Leu-
Gly-Lys-Leu-Ser-Ala-Ile-Pro-Asn-Asp-Thr-
Ala-Ala-Lys-Leu-Gln-Ala-Val-Lys-Asp-Lys-
Ala-Arg-Gln-Ala-Asn-Asp-Thr-Ala-Lys-Asp-
Ala-Arg-Gln-Ala-Asn-Asp-Thr-Ala-Lys-Asp-
Ala-Arg-Gln-Ala-Asn-Asp-Thr-Ala-Lys-Asp-
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val-Ala-Lys-Glu-Ala-Lys-Asp-Leu-Ala-His-
Glu-Ala-Thr-Lys-Leu-Ala-Thr-Gly-Pro-Arg-
Gly-Leu-Lys-Glu-Asp-Ala-Lys-Gly-Cys-
Leu-Gln-Lys-Ser-Phe-Arg-Ile-Leu-Asp-Glu-
Ala-Lys-Lys-Leu-Ala-Asn-Asp-Val-Lys-Glu-
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Asp-Asn-Leu-Lys-Lys-Asn-Ile-Ser-Glu-Ile-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ala-Asp-Ala-Val-Arg-Val-Ile-Thr-Phe-Thr-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leu-Asp-Glu-Ala-Lys-Asn-Ile-Ser-Phe-Asn-
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                                                                                                                          Ala-Thr-Arg-Asp-Leu-Arg-Asp-Phe-Met-Ser-
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1999-326542 [27]
N-ESDB: AAXX59768
C Human Laminin alpha 2 subunit.
AAX15460 Protein DEENE
205A: 159R; 162N; 183D; 0 B; 162C; 11
246L; 184K; 46 M; 103F; 173P; 194S; 19
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AT:
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2431
2441
2451
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Brunken W; Burgeson R E; Champliaud
(GEHO) GEN HOSPITAL CORP.
***WO 9919348 A1 19990422
WO 1998-US21391 19981008
US 1997-61609 19971010
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AAX15460 Protein DGENE
Purified laminin 12 useful fo
           1 Met-Pro-Gly-Ala-Ala-Gly-Val-Leu-Leu-Leu-
11 Leu-Leu-Ser-Gly-Gly-Leu-Gly-Gly-Val-
21 Gln-Ala-Gln-Arg-Pro-Gln-Gln-Gln-Arg-Gln-
31 Ser-Gln-Ala-His-gln-Gln-Arg-Gly-Leu-Phe-
31 Ser-Gln-Ala-His-gln-Gln-Arg-Gly-Leu-Phe-
41 Pro-Ala-Val-Leu-Asn-Leu-Ala-Thr-Cys-Gly-Glu-
42 Pro-Ala-Val-Leu-Asn-Leu-Ala-Thr-Cys-Gly-Glu-
43 Lys-Gly-Pro-Glu-Met-Tyr-Cys-Lys-Leu-Val-
44 Pro-Gln-Cys-Arg-Ile-Cys-Asn-Gln-Asn-Ser-
45 Pro-Gln-Cys-Arg-Ile-Cys-Asn-Gln-Asn-Ser-
46 Pro-Gln-Cys-Arg-Ile-Cys-Asn-Gln-Asn-Ser-
47 Pro-Gln-Cys-Arg-Ile-Cys-Asn-Gln-Asn-Ser-
48 Pro-Gln-Cys-Arg-Ile-Cys-Asn-Gln-Asn-Ser-
49 Ser-Asn-Pro-Asn-Gln-Arg-His-Pro-Ile-Thr-
40 San-Ala-Ile-Asp-Gly-Lys-Asn-Gly-Ile-Glu-
41 Val-Lys-Ala-Ala-Asn-Ser-Pro-Arg-Pro-Gly-
41 Val-Lys-Ala-Ala-Asn-Ser-Pro-Arg-Pro-Gly-
41 Val-Thr-Asp-Thr-Glu-Gly-Fro-Pro-Ser-
41 Val-Thr-Asp-Thr-Glu-Gly-Fro-Pro-Ser-
41 Val-Thr-Asp-Thr-Glu-Gly-Fro-Pro-Ser-
41 Val-Thr-Asp-Thr-Glu-Gly-Fro-Pro-Ser-
41 Val-Thr-Asp-Thr-Gly-Pro-Pro-Ser-
41 Val-Thr-Asp-Thr-Gly-Fro-Hu-Thr-Leu-Tyr-
41 Val-Thr-Asp-Thr-Gly-Fro-Hu-Thr-Leu-Tyr-
41 Val-Thr-Asp-Thr-Gly-Fro-Pro-Pro-Ser-
41 Val-Thr-Asp-Thr-Gly-Fro-Pro-Pro-Ser-
41 Val-Thr-Asp-Thr-Gly-Fro-Hu-Thr-Leu-Tyr-
41 Val-Thr-Asp-Thr-Gly-Fro-Hu-Thr-Leu-Tyr-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-Vys-Thr-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-Vys-Thr-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-Asp-Thr-Glu-Val-Ile-His-
41 Val-Thr-
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Gln-Lys-Gln-Ala-Asn-Ile-Ser-Ile-Val-Asp-
Ile-Asp-Thr-Asn-Gln-Glu-Glu-Asn-Ile-Ala-
Thr-Ser-Ser-Ser-Gly-Asn-Asp-Phe-Gly-Leu-
Asp-Leu-Lys-Ala-Asp-Asp-Lys-Ile-Tyr-Phe-
527-534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPYRIGHT 2004 The Thomson Corp on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for promoting tissue repair and promoting
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231 Glu-Leu-Kou-Glu-Phe-Thr-Ser-Ala-Arg-Tyr-
241 III-Arg-Leu-Arg-Phe-Gln-Arg-III-Arg-Thr-
251 Leu-Asn-Ala-Asp-Leu-Met-Met-Phe-Ala-His-
251 Lys-Asp-Pro-Arg-Glu-II-Asp-Pro-II-Val-
251 III-Ser-Val-Gly-Glu-II-Asp-Pro-II-Val-
251 III-Ser-Val-Gly-Gly-Met-Cys-II-Cys-Glu-
251 III-Ser-Val-Gly-Gly-Met-Cys-II-Cys-Glu-
251 Gly-His-Ala-Arg-Tyr-Tyr-Ser-Cys-Sp-Gln-
251 Cys-Cys-Pro-Gly-Phe-His-Gln-Lys-Pro-II-
251 Gly-His-Ala-Arg-Tyr-Tyr-Asp-Glu-Asn-Val-Ala-
252 Glu-Glu-Cys-Tyr-II-Cly-Yeb-His-Gly-II-Asn-Val-Ala-
253 Glu-Glu-Cys-Tyr-II-Cly-Yeb-Leu-Asn-II-Asn-Cys-
254 Cys-Thr-Gln-Asn-In-Ala-Gly-II-Asn-Cys-
255 Glu-Thr-Cys-Tyr-II-Cly-Yeb-Lys-Ala-
256 Lys-Glu-Ala-Cys-Tyr-II-Asp-Gly-Asn-Val-Asn-
257 Cys-Thr-Gln-Asn-In-Ala-Gly-II-Asn-Cys-
258 Glu-Thr-Cys-Tyr-II-Cly-Yeb-Lys-II-Asn-Cys-
259 Glu-Thr-Cys-Tyr-II-Cly-Yeb-Cys-Asp-Pro-II-Asp-Cly-
250 Lys-Gln-Pro-Cys-His-Cys-Asp-Pro-II-Cly-
251 Cys-Gln-Pro-Cys-His-Cys-Asp-Cys-
252 Cys-Fris-Gly-Leu-Gly-Pro-Cys-II-Cys-Lys-Ala-
253 Lys-His-Ala-Arg-Arg-Gly-Leu-Ala-Pro-Gly-
254 Cys-Fright-Gly-Pro-Cys-II-Cys-Lys-Ala-
255 Lys-Ser-Gly-Leu-Gly-Pro-Cys-II-Cys-Lys-Ala-
257 Cys-Pro-Gly-Phe-Phe-Asn-Leu-Glu-Asp-Met-
258 Cys-Cys-Pro-Tyr-Pro-Asp-Cys-Cys-
259 Lys-Ser-Gly-Phe-Phe-Asn-Leu-Gln-Gly-Pro-Gly-
250 Lys-Ser-Gly-Phe-Phe-Asn-Leu-Gln-Gly-Pro-Gly-
251 Lys-Gly-Cys-Asp-Glu-Cys-Phe-Cys-
252 Ser-Gly-Pro-Tyr-Leu-Thr-Tyr-Gly-Lys-II-Cys-Lys-Phe-
253 Tyr-Trp-Thr-Tyr-Gly-Cys-Asp-Glu-Cys-Phe-
254 Ser-Gly-Thr-Pro-Tyr-Leu-Thr-Asp-Leu-Pro-His-
255 Leu-Gly-Asn-Lys-Gln-Gln-Gln-Gln-Asp-Asp-
256 Leu-Asp-Ser-Pro-Ala-Pro-Glu-Cys-Phe-
257 Asn-Ala-Glu-Glu-Glu-Gls-Glu-Cys-Phe-
258 Leu-Gly-Asn-Lys-Leu-Pro-His-Ser-Ser-
259 Leu-Gly-Asn-Lys-Glu-Glu-Glu-His-Pro-Tyr-
250 Leu-Cys-Ser-Ple-Phe-Thr-II-Ser-Ple-Phe-
251 Asn-Val-Leu-Leu-Lys-Glu-Glu-His-Pro-Val-Asr-
252 Ser-Gly-Met-Asp-Clu-Glu-His-Pro-Val-Asr-
253 Tyr-Trp-Thr-Tyr-Gly-Fro-Gln-Gln-Gln-Asp-Clu-
254 Leu-Gly-Asn-Lys-Glu-Gln-Gln-Asp-Clu-
255 Leu-Gly-Asn-Lys-Glu-Gln-Asp-Clu-
256 Leu-Asp-Ser-Pro-Ala-Pla-
257 Leu-Gly-Asn-Lys-Glu-Gly-Asp-Pla-
258 Leu-Gly-Asn-Lys-Glu-Gly-Asp-Pla-
259
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301	221 231 241 251 251 261 271 281 291	111 121 131 141 151 151 161 171 171 191 191 201	991 001 001 001 001 001 001 003 003 003 00	7781 7791 8821 8821 8831 8851 8861 8871 9911 9921 9931
-His-Glu-11e-Glu-Met-Tir-Glu-Lys-Gl -Lys-Tyr-Tyr-Gly-Asp-Asp-Pro-Arg-Va -Arg-Thr-Val-Thr-Arg-Glu-Asp-Pro-Le- -Arg-Thr-Val-Thr-Arg-Glu-Asp-Phe-Le- -Iie-Leu-Tyr-Asp-Iie-His-Tyr-Iie-Le- -Lys-Ala-Thr-Tyr-Gly-Asn-Phe-Met-Ar	t-Asp-Leu-Met-Arg-Glu-Asp-Leu-His-L u-Pro-Phe-Tyr-Trp-Lys-Leu-Pro-Glu-G e-Glu-Gly-Lys-Lys-Leu-Met-Ala-Tyr-G y-Lys-Leu-Lys-Tyr-Ala-Ile-Tyr-Phe-G a-Arg-Glu-Glu-Thr-Gly-Phe-Ser-Thr-I a-Arg-Glu-Glu-Thr-Gly-Phe-Gly-T 0-Thr-His-Ala-Arg-Ile-Ile-Val-Arg-T t-Ala-Ala-Pro-Leu-Tle-Gly-Gly-Gly-T	o-Gly-Thr-Asp-Ala-Thr-Thr-Cys- u-Thr-Lys-Lys-Cys-Ser-Cys-Ser- u-Gly-Gln-Cys-Thr-Cys-Lys-Val- u-Gly-11e-His-Cys-Asp-Arg-Cys- y-Lys-Phe-Gly-Leu-Asp-Ala-Lys- u-Gly-Cys-Ser-Ser-Cys-Tyr-Cys- r-Thr-Thr-Gln-Cys-Ser-Glu-Ala- u-I1e-Arg-Thr-Trp-Val-Thr-Leu- u-Gln-Thr-Tle-Leu-Pro-Leu-Val- a-Leu-Gln-His-Thr-Thr-Thr-Lys- l-Phe-Gln-His-Pro-Glu-I1e-Val-	r-Phé-Gly-Ser-Lys-Ser-Phé-Asp-Cys-Gl u-Ser-Gly-Gln-Cys-Trp-Cys-Gln-Pro-Gl L-Thr-Gly-Lys-Lys-Cys-Asp-Arg-Cys-Al s-Gly-Tyr-Phe-Asn-Phe-Gln-Glu-Gly-Gl s-Gly-Tyr-Phe-Asn-Phe-Gln-Glu-Gly-Gl s-Thr-Ala-Cys-Glu-Cys-Ser-His-Lau-Gl n-Asn-Cys-Asp-Pro-Lys-Thr-Gly-Glu-Ly e-Cys-Pro-Pro-Asn-Thr-11a-Gly-Glu-Ly e-Cys-Pro-Pro-Asn-Thr-Gly-Cys-Lys-Ala-Pro-Ser-Tlp-Gl-Cys-Ala-Pro-Ser-Lys-Cys-Ala-Pro-Ser-Thr-Val-Gly-Ser-Leu-Asp-Ph n-Cys-Ser-Thr-Val-Gly-Ser-Leu-Asp-Ph n-Cys-Ser-Thr-Val-Gly-Gn-Cys-Ala-Tys-Cys-Asn-Val-Asn-Thr-Gly-Gn-Cys-Asn-Tys-Cys-Tys-Cys-Tys-Cys-Tys-Cys-Tys-Cys-Tys-Cys-Tys-Cys-Cys-Cys-Cys-Tys-Cys-Cys-Tys-Cys-Cys-Cys-Cys-Cys-Cys-Cys-Cys-Cys-C	Gly-Gly-Pro-Tyr-Cys-Asp-Lys-Cys-Leu-Pro- Gly-Pho-Tyr-Gly-Glu-Pro-Thr-Lys-Gly-Thr- Ser-Glu-Asp-Cys-Gln-Pro-Cys-Ala-Cys-Pro- Leu-Asn-Ile-Pro-Ser-Asn-Asn-Phe-Ser-Pro- Leu-Asn-Ile-Pro-Ser-Asn-Asn-Phe-Ser-Pro- Thr-Cys-His-Leu-Asp-Arg-Ser-Leu-Gly-Leu- Ile-Cys-Gly-Cys-Pro-Val-Gly-Iyr-Ihr- Gly-Pro-Arg-Cys-Gly-Cys-Pro-Val-Gly-Iyr-Ihr- Gly-Pro-Arg-Cys-Gln-Pro-Ser-Val-Pro-Gly-Gly- Tyr-Phe-Gly-Gln-Pro-Cys-Asn-Asp-Asn-Asn- Leu-Asp-Phe-Ser-Ile-Pro-Gly-Ser-Cys-Asn- Leu-Asp-Phe-Ser-Ile-Pro-Gly-Ser-Cys-Asp- Ser-Leu-Ser-Gly-Tyr-Phe-Gly-Asp-Ala-Val- Cys-Ala-Asp-Gly-Tyr-Phe-Gly-Asp-Ala-Val- Asp-Ala-Lys-Asn-Cys-Gln-Pro-Cys-Asp- His-Ser-Gln-Thr-Gly-Ser-Phe-Ser-Glu-Vys-Arg- Ala-Asn-Val-Gly-Thr-Phe-Gly-Leu-Gln-Cys- Cys-Nasp-Ala-Gly-Gly-Tyr-De-Gly-Ser-Ile- Cys-Asp-Ala-Cys-Asp-Ala-Cys- Asn-Ala-Gly-Gly-Ser-Phe-Ser-Glu-Vys-Asp- Cys-Nasp-Ala-Gly-Gly-Tyr-Phe-Gly-Leu-Gln-Ser- Cys-Nasp-Ala-Gly-Gly-Tyr-Phe-Gly-Leu-Gln-Ser- Cys-Nasp-Ala-Cys-Asp-Ala-Cys- Ala-Asn-Val-Gly-Thr-Phe-Gly-Leu-Gln-Ser- Ala-Asn-Val-Gly-Cys-Val-Cys- Ala-Asn-Val-Gly-Thr-Phe-Gly-Leu-Gln-Ser- Ala-Asn-Val-Gly-Gly-Thr-Phe-Gly-Leu-Gln-Ser- Ala-Asn-Val-Gly-Gly-Thr-Phe-Gly-Leu-Gly-Ser- Ala-Asn-Val-Gly-Gly-Thr-Phe-Gly-Gly-Thr-Phe-Gly

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1311 Lys-Pro-11e-Gly-Leu-Trp-Asn-Phe-Arg-Glu-
1321 Lys-Glu-Gly-Asp-Cys-Lys-Gly-Cys-Thr-Val-
1321 Ser-Pro-Gln-Val-Glu-Asp-Ser-Glu-Gly-Thr-
1331 Ser-Pro-Gln-Val-Glu-Gly-Ser-Glu-Gly-Thr-
1331 Ile-Gln-Phe-Asp-Gly-Glu-Gly-Tyr-Ala-Leu-
1341 Ile-Gln-Phe-Asp-Gly-Glu-Gly-Tyr-Ala-Leu-
1351 Val-Ser-Arg-Pro-11e-Arg-Trp-Tyr-Pro-Asn-
1351 Val-Ser-Arg-Asp-Leu-Arg-Asp-Phe-Met-Ser-
1371 Phe-Ser-Ser-Ser-Ala-Leu-Leu-Met-Tyr-Leu-
1371 Phe-Ser-Ser-Ser-Ala-Leu-Leu-Met-Tyr-Leu-
1371 Ala-Thr-Arg-Asp-Leu-Arg-Asp-Phe-Met-Ser-
1371 Ala-Thr-Arg-Asp-Leu-Arg-Asp-Gly-
1371 Val-Glu-Ileu-Thr-Asp-Gly-Met-Ala-Ser-
1471 Val-Val-Ser-Asp-Gly-Met-Ala-Ser-
1471 Val-Val-Ser-Asp-Gly-Met-Asp-Gly-
1471 Val-Val-Ser-Asp-Gly-Met-Asp-
1471 Val-Val-Ser-Asp-Met-Asp-
1471 Val-Val-Ser-Asp-
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71 Lys-Seu-Ala-Asp-Ser-Val-Ala-Lys-Thr-Asn-
71 Lys-Ser-Lys-Asn-Lys-Ser-Lys-Asn-Lys-
81 Ala-Val-Val-Asp-Ala-Asp-Pro-Ser-Lys-Asn-Lys-
91 Ile-Ile-Ala-Asp-Ala-Asp-Ala-Thr-Val-Lys-
91 Ile-Ile-Ala-Asp-Ala-Asp-Ala-Thr-Val-Lys-
91 Asn-Leu-Glu-Gln-Glu-Ala-Asp-Asg-Leu-Ile-
11 Asp-Lys-Leu-Lys-Fro-Ile-Lys-Glu-Leu-Clu-
11 Asp-Lys-Leu-Lys-Fro-Ile-Ser-Glu-Ile-
21 Asp-Asn-Leu-Lys-Lys-Asn-Ile-Ser-Glu-Ile-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lys-Glu-Leu-Ile-Asn-Gln-Ala-Arg-Lys-Gln-Ala-Asn-Ser-Ile-Lys-Val-Ser-Ser-Gly-Gly-Asp-Cys-Ile-Arg-Thr-Tyr-Lys-Pro-Glu-Ile-Lys-Cly-Ser-Tyr-Asn-Asn-Ile-Val-Asn-Val-Lys-Gly-Ser-Thr-Ala-Val-Ala-Asp-Asn-Leu-Phe-Tyr-Leu-Gly-Ser-Ala-Lys-Asn-Leu-Phe-Tyr-Leu-Gly-Ser-Ala-Lys-Asn-Leu-Phe-Tyr-Leu-Gly-Ser-Ala-Lys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phe-Ile-Asp-Phe-Lou-Ala-Ile-Glu-Met-Arg-
lys-Gly-Lys-Val-Ser-Phe-Leu-Trp-Asp-Val-
Gly-Ser-Gly-Val-Gly-Arg-Val-Glu-Tyr-Pro-
Asp-Leu-Thr-Ile-Asp-Asp-Ser-Tyr-Trp-Tyr-
Arg-Ile-Val-Ala-Ser-Arg-Thr-Gly-Arg-Asn-
Gly-Thr-Ile-Ser-Val-Arg-Ala-Leu-Asp-Gly-
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Asp-Leu-Leu-Arg-Thr-Leu-Asn-Asp-Thr-Leu-
Gly-Lys-Leu-Ser-Ala-Ile-Pro-Asn-Asp-Thr-
Ala-Ala-Lys-Leu-Gln-Ala-Val-Lys-Asp-Lys-
Ala-Arg-Gln-Ala-Asn-Asp-Thr-Ala-Lys-Asp-
Val-Leu-Ala-Gln-Ile-Thr-Glu-Leu-His-Gln-
Val-Leu-Ala-Gln-Ile-Thr-Glu-Leu-His-Gln-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pro-Lys-Ala-Ser-Ile-Val-Pro-Ser-Thr-His-
His-Ser-Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile-
Leu-Asp-Val-Asp-Ala-Asn-Ala-Met-Leu-Phe-
Ile-Asp-Thr-Asn-Gln-Glu-Glu-Asn-Ile-Ala-
Thr-Ser-Ser-Ger-Gly-Asn-Asn-Phe-Gly-Leu-
Asp-Leu-Lys-Ala-Asp-Asp-Lys-Ile-Tyr-Phe-
527-534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Val-Gly-Gly-Leu-Thr-Gly-Lys-Leu-Lys-Lys-
Ala-Asp-Ala-Val-Arg-Val-Ile-Thr-Phe-Thr-
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Ala-Lys-Lys-Leu-Ala-Asn-Asp-Val-Lys-Glu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gly-Leu-Leu-Lys-Glu-Asp-Ala-Lys-Gly-Cys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glu-Ala-Thr-Lys-Leu-Ala-Thr-Gly-Pro-Arg-
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HITS

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ANSWER 33 OF 36 DGENE AAR71730 Protein

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IN PA PA PI AI DT CR CR CR DESC
    HITS
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125
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1999-519628 [44]
N-PSDB: AAZ33446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate cancer-associated AAY46244 Protein DGENE 29 A; 5 R; 8 N; 7 D; 0 B; 15 40 L; 6 K; 5 M; 12 E; 27 P; 28 304
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New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for therapeutic agents

Specht T; Hinzmann B; Schmitt A; Pilarsky C; Dahl E; Rosenthal A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANSWER 32 OF 36 I
AAY48244 Protein
New nucleic acid 6
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DE 1998-19811193
111 Cys-Leu-Phe-Ser-Leu-Ile-Gly-Asn-Met-Gly-
121 Ala-Phe-Met-Val-Ala-Leu-Ile-Gly-Ser-Leu-Leu-
121 Arg-Tyr-Gly-Gln-Leu-Leu-Glu-Gln-Ser-Arg-
131 Arg-Tyr-Gly-Gln-Gln-Gln-Gln-Ser-Arg-
141 His-Ser-Trp-Val-Asn-Thr-Thr-Ala-Leu-Ile-
151 Thr-Gly-Ysn-Phe-Gln-Val-Asp-His-Ala-Arg-
151 Ser-Leu-His-Tyr-Val-Gly-Ala-Gly-Leu-Leu-
161 Val-Gly-Asn-Phe-Gln-Val-Ala-Gly-Val-Ala-
171 Ser-Leu-His-Tyr-Val-Gly-Ala-Gly-Val-Ala-
171 Ser-Leu-His-Tyr-Val-Gly-Ala-Gly-Val-Ala-
172 His-Cys-Ala-Leu-Ser-Tyr-Gln-Gly-Ala-Phe-Ile-
173 His-Gly-Eleu-Ala-Val-Ile-Ala-Phe-Ile-
174 Ala-Leu-Cys-Glu-Trp-Val-Cys-Val-Ile-Phe-Val-
175 Glu-Phe-Gly-Ala-Val-Gly-Phe-Ser-Tyr-
176 Glu-Phe-Gly-Ala-Val-Ser-Ser-Asp-Thr-Leu-
177 Val-Ala-Ala-Leu-Gln-Pro-Thr-Phe-Ser-Thr-
178 Ser-Thr-His-Leu-Ser-Ser-Gly-Ser-Thr-
179 Ser-Thr-His-Leu-Asn-Cys-Ala-Pro-Glu-Ser-
171 Ser-Thr-His-Leu-Asn-Cys-Ala-Pro-Glu-Ser-
172 Ser-Thr-His-Leu-Asn-Cys-Ala-Pro-Glu-Ser-
173 Ser-Thr-His-Leu-Asn-Cys-Ala-Pro-Glu-Ser-
174 Ala-Ala-Het-Ile
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Gly-Pro-Pro-Pro-Leu-Pro-His-Leu-Pro-Leu-
Val-Leu-Pro-Pro-Thr-Pro-Pro-Pro-Pro-Trp-
                                                                                                                                                                                                                                                                                                                                                                                                          Asp-Pro-Ala-Glu-Gln-Gly-Gly-Pro-Lys-Thr-
Cys-Cys-Thr-Leu-Asp-Asp-Val-Pro-Leu-Ile-
Ser-Lys-Cys-Gly-Ser-Tyr-Pro-Pro-Glu-Ser-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leu-Pro-Ser-Leu-Met-Thr-Ala-Trp-Ile-Leu-
Leu-Pro-Val-Ser-Leu-Ser-Ala-Phe-Ser-Ile-
Thr-Gly-Ile-Trp-Thr-Val-Gln-Pro-Lys-Ala-
Val-Met-Asn-His-His-Val-Cys-Pro-Val-Glu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asn-Trp-Ser-Tyr-Asn-Glu-Ser-Cys-Pro-Pro-
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Others
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301 Glu-Thr-Cys-Thr-Asp-Gly-Phe-Phe-Arg-Pro-410 Lyg-Gly-Val-Ser-Pro-Asn-Tyr-Pro-Asp-Gly-Val-Cys-Asp-Pro-11e-Gly-421 Ser-Lu-Asn-Glu-Val-Cys-Asp-Pro-11e-Gly-421 Ser-Lu-Asn-Glu-Val-Cys-Val-Lyg-Asp-Glu-Val-Cys-Sep-Fro-Gly-441 Ser-Cys-His-Cys-Lyg-Thr-Gly-Phe-Gly-441 Ser-Cys-His-Cys-Lyg-Thr-Gly-Phe-Gly-441 Ser-Cys-His-Cys-Lyg-Thr-Gly-Phe-Gly-451 Val-Ser-Cys-His-Cys-Lyg-Sep-Cys-Lyg-Sep-Cys-Lyg-Sep-Cys-Lyg-Sep-Cys-Lyg-Sep-Cys-Lyg-Sep-Cys-Lyg-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-Sep-Cys-
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001 Arg-Tle-Glu-Asn-Ala 001 Asp-Leu-Leu-Arg-Thi 021 Gly-Lys-Leu-Ser-Ala 031 Ala-Ala-Lys-Leu-Glr 041 Ala-Arg-Gln-Ala-Asr 051 Val-Leu-Ala-Gln-Ile 061 Asn-Leu-Ala-Gly-Leu 071 Lys-Leu-Ala-Asp-Sez	1 Asn-Asp-Ser-Ala-Lys 1 Leu-Asp-Glu-Ala-Lys 1 Ala-Thr-Ala-Ala-Ply 1 Ala-Thr-Ala-Ala-Ply 1 11e-Lys-Asp-Tyr-Ile 1 Val-Ala-Thr-Lys-Glu-Ala 1 Gly-Leu-Leu-Lys-Glu- 1 Gly-Leu-Lys-Ser-Phe 1 Ala-Lys-Lys-Leu-Ala 1 Asn-Glu-Asp-His-Leu- 1 Asn-Glu-Asp-His-Leu-	781 Asn-Lys-Val Asp-Asp 791 Arg-Clu-Ala-Thr-Asp 801 Asn-Arg-Leu-Phe-Al 801 Asn-Arg-Leu-Phe-Al 801 Asn-Arg-Leu-Phe-Al 801 Met-Thr-Ala-Leu-Glu 801 Mr-Leu-Lys-Glu-Gly 801 Glu-Ala-Asn-Arg-Leu 805 Ser-11e-11e-Asp 801 Thr-Lys-Leu-Pro-Phe 801 Thr-Lys-Leu-Pro-Phe 801 Ile-Lys-Asp-Arg-Lys 801 Ser-Gln-Ala-Glu-Se	21 Gly-Gly-Ser-Cys 21 Gly-Gly-Ser-Cys 31 Pro-Tyr-Gly-Ser- 41 Pro-Tyr-Gly-Ser- 41 Pro-Tyr-Gly- 51 Gly-Ala-Thr-Gly- 61 Leu-Leu-Leu-Gly- 61 Leu-Leu-Leu-Gly- 61 Pro-Leu-Pro-Ala- 61 Gly-Leu-Glu-Asn- 61 Gly-Glu-Glu-Glu-Asn- 61 Gly-Glu-Glu-Glu-Glu- 61 Gly-Glu-Glu-Glu- 61 Gly-Glu-Glu-Glu- 61 Gly-Glu-Glu-Glu- 61 Gly-Glu-Glu-Asn-Ibu- 61 Gly-Glu-Glu-Glu- 61 Gly-Glu-Glu-Glu- 61 Gly-Asn-Ibu- 61 Gly-Asn-Ibu- 61 Glu-Asp-Glu-Met- 61 Glu-Asp-Glu-Leu- 61 Glu-Asp-Glu-Leu- 61 Glu-Asp-Glu-Leu- 61 Glu-Asp-Glu-Leu- 61 Glu-Asp-Glu-Glu- 61 Glu-Asp-Glu-Leu- 61 Glu-Asp-Glu-Glu- 61 Glu-Asp-Glu-Leu- 61 Glu-Asp-Glu-Glu- 61 Asp-Leu-Asp-Glu- 61 Asp-Leu-Asp-Glu- 61 Asp-Leu-Asp-Glu- 61 Asp-Leu-Asp-Glu- 61 Asp-Leu-Asp-Glu-
a-Asp-Ala- r-Leu-Asn- a-Ile-Pro- n-Ala-Val- n-Asp-Thr- e-Thr-Glu- u-Lys-Lys- u-Val-Ala-	a-Val-Leu-Asp-Gly-I s-Asp-1le-Ser-Phe-A e-Lys-Ala-Tyr-Ser-A e-Asp-Glu-Ala-Glu-L a- Lys-Asp-Glu-Ala-H u-Ala-Thr-Gly-Pro-A u-Asp-1a-Lys-Gly-C a-Asp-1la-Lys-Gly-C a-Asp-Gly-Leu-Lys-G u-Asp-Gly-Leu-Lys-G	Ala-Trp-Asp-Leu- lys-Tle-Arg-Clu- Val-Asn-Cln-Lys- Lys-Lys-Glu- Arg-Gln-Tle-Glu- Asn-Asp-Glu-Ile- Val-Glu-Asp-Ile- Mer-Ser-Glu-Glu- Asp-Leu-Ser-Glu-Lys- Leu-Ala-Glu-Lys-	reducys-galu-cyg-Asp Pro-Val-Pro-Cys-Asp - Cys-Cys-Asp-Gly-Cys- - Lys-Cys-Asp-Gly-Cys- - Lys-Cys-Asp-Gly-Cys- - Lys-Cys-Asp-Glu-Cys-Thr-Gly- - Leu-Ala-Asp-Clu-Cus- - Clu-Asp-Leu-Cys- - Clu-Asp-Leu-Cys- - Clu-Asp-Clu-Leu-Cys- - Clu-Asp-Clu-Leu-Cys- - Clu-Asp-Clu-Asp-Clu-Leu-Asp- - Lys-Ser-Leu-Gly-Glu-Asp- - Lys-Ser-Leu-Cys-Leu-Asp- - Clu-Asp-Clu-Asp-Clu-Leu-Asp- - Clu-Asp-Clu-Leu-Asp- - Clu-Asp-Clu-Leu-Asp-Clu-Lys- - Clu-Asp-Clu-Lys-Clu-Cu-Lys-Clu-Ly

SIIH 271 Leu-Asp-Val-Asp-Ala-Ment-Leu-Phe272 Leu-Asp-Val-Asp-Ala-Ment-Leu-Phe273 Ala-Asp-Ala-Val-Asp-Ala-Ment-Leu-Phe274 Ala-Asp-Ala-Val-Asp-Val-Asp-Leu-Lys-Lys275 Ala-Asp-Ala-Val-Asp-Val-Isle-Thr-Phe-Thr276 Idy-Cys-Met-Gly-Glu-Thr-Tyr-Phe-Asp-Asp277 Lys-Pro-Isle-Gly-Leu-Trp-Asn-Phe-Arg-Glu278 Lys-Pro-Isle-Gly-Leu-Trp-Asn-Phe-Arg-Glu279 Lys-Pro-Isle-Gly-Leu-Trp-Asn-Phe-Arg-Glu270 Lys-Pro-Isle-Asp-Gly-Glu-Gly-Tyr-As-Leu271 Lys-Pro-Isle-Asp-Gly-Gly-Gly-Tyr-As-Leu271 Le-Ser-Arg-Pro-Isle-Arg-Thr271 Phe-Ser-Ser-Asp-Leu-Arg-Asp-Phe-Met-Ser271 Phe-Ser-Ser-Ser-Ala-Leu-Leu-Met-Tyr-Leu271 Phe-Ser-Ser-Ser-Ala-Leu-Leu-Met-Arg-Thr271 Phe-Ser-Ser-Asp-Leu-Arg-Asp-Phe-Met-Ser271 Phe-Ser-Ser-Asp-Leu-Arg-Asp-Phe-Met-Ala-Ser271 Phe-Ser-Ser-Asp-Leu-Gly-Ser-Gly-Met-Ala-Ser272 Ala-Glu-Leu-Thr-Asp-Gly-His-Isle-Tyr-Phe273 Id-Glu-Lys-Gln-Ala-Asp-Isle-Ser-Arg-Isle274 Isle-Tyr-Phe-Thr-Leu-Ser-Arg-Isle275 Isle-Tyr-Ser-Ser-Ser-Gly-Asn-Phe-Gly-Leu276 Asp-Leu-Lys-Ala-Asp-Lys-Isle-Tyr-Phe277 S27-534 81 Asn-Leu-Leu-Phe-Tyr-Leu-Gly-Ser-Ala-Lys91 Phe-Ile-Asp-Phe-Leu-Ala-Ile-Glu-Met-Arg91 Lys-Gly-Lys-Val-Ser-Phe-Leu-Typ-Asp-Val91 Lys-Gly-Lys-Val-Ser-Phe-Leu-Typ-Asp-Val91 Gly-Ser-Gly-Val-Gly-Arg-Val-Glu-Tyr-Pro91 Asp-Leu-Thr-Ile-Asp-Asp-Ser-Tyr-Tyr921 Asp-Leu-Thr-Ile-Asp-Asp-Ser-Tyr-Gly-Arg-Asn931 Gly-Thr-Ile-Ser-Val-Arg-Ala-Leu-Asp-Gly931 Gly-Thr-Ile-Ser-Val-Arg-Ala-Leu-Asp-Gly931 Fro-Lys-Ala-Ser-Ile-Val-Pro-Ser-Thr-His931 His-Ser-Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile932 Thr-Ile-Ser-Val-Arg-Ala-Leu-Asp-Gly933 Thr-Ile-Ser-Val-Arg-Ala-Leu-Asp-Gly934 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile935 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile935 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile935 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile935 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile935 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile935 Thr-Ser-Pro-Pro-Gly-Tyr-Thr-Ile-Gly-Gly-Asp-Cys-Ile-Arg-Thr-Tyr-Lys-Pro-Glu-Ile-Lys-Lys-Gly-Ser-Tyr-Asn-Asn-Ile-Val-Val-Asn-Val-Lys-Thr-Ala-Val-Ala-Asp-Ala -Val -Val - Lys - Asp - Pro - Ser - Lys - Asn - Lys - Ile - Ile - Ala - Asp - Ala - Thr - Val - Lys - Ile - Ile - Ala - Asp - Ala - Thr - Val - Lys - Asn - Leu - Glu - Glu - Ala - Asp - Arg - Leu - Ile - Asp - Lys - Glu - Leu - Glu - Asp - Lys - Glu - Leu - Glu - Asp - Lys - Glu - Leu - Glu - Asp - Lys - Glu - Leu - Glu - Asp - Lys - Glu - Leu - Glu - Asp - Lys - Glu - Leu - Glu - Asp - Lys - Glu - Leu - Glu - Asp - Lys - Glu - Gl Lys-Glu-Leu-Ile-Asn-Gln-Ala-Arg-Lys-Gln-Ala-Asn-Ser-Ile-Lys-Val-Ser-Val-Ser-Ser-Asp-Asn-Leu-Lys-Lys-Asn-Ile-Ser-Glu-Ile-

FEATURE TABLE: Key	: Location Qualifier +=========+	Qualifier	FEATURE TABLE: Key Location Qualifier
	112298	note	"region encoded by AAQ86480"
Peptide Domain	123286	note label	"Signal peptide" Domain VI
	-	note	"predicted to form globular
Modified-site 15557	15557	note	"N-linked glycosylation site"
Modified-site(8991	18991	note	"N-linked glycosylation site"
Domain	1287527	label note	Domain V "contains four and one half
			Cystein-rich EGF-like repeats, predicted to have rigid

Modified-site	Modified-site	Domain Domain	Modified-site Modified-site Domain	Modified-site Modified-site Modified-site Modified-site Modified-site Domain
22402242 note 23602362 note 24352471 note 247524671 note 257512553 note 255612550 note 264612550 note 264612550 note 28932951 note 28932951 note	115971599 note 116141616 note 117001702 note 118101812 note 119101923 note 119101923 note 119101923 note 119201922 note 120172019 note 120282030 note 120282030 note 120282031 note	11801573 label note 15742153 label note	1746748 note 10611063 note 11761379 label	303305 note 363365 note 380382 note 470472 note 528723 label 17241175 label
	"N-linked glycosylation site" "N-lin	four Cystein-ric epeats, predicte gid rod-like I B-type chains, le coiled-coil	ich EGF-like rep to have rigid structure" glycosylation s glycosylation s a to form globul	"N-linked glycosylation site" "Domain IVb "predicted to form globular structure" Domain IIb

125

ANSWER 34 OF 36 DGENE COPYRIGHT 2004 The Thomson Corp on STN AAR82244 Protein DGENE Production of fibrinogen in transgenic mammals - by introducing DNA segments into the germ line of a non-human mammal and collecting milk from female progeny.

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PI AII DT LA OS CR CR AN
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English
1995-320582 [41]
N-PSDB: AATO3853
Human fibrinogen A-
AAR82244 Protein
24 A; 42 R; 29 N; 3
33 L; 40 K; 12 M; 2
644
  71 Lys-Gly-Leu-Ile-Asp-Glu-Val-Asn-Gln-Asp-
81 Phe-Thr-Asn-Arg-Ile-Asn-Lys-Leu-Lys-Asn-
91 Ser-Leu-Phe-Glu-Tyr-Gln-Lys-Asn-Sn-Lys-
101 Asp-Ser-His-Ser-Leu-Thr-Thr-Asn-Ile-Met-
101 Asp-Ser-His-Ser-Leu-Thr-Thr-Asn-Ile-Met-
101 Asp-Ser-His-Ser-Leu-Thr-Thr-Asn-Ile-Met-
101 Glu-Ile-Leu-Arg-Gly-Asp-Phe-Ser-Ser-Ala-
111 Glu-Ile-Leu-Arg-Gly-Asp-Phe-Ser-Ser-Ala-
112 Asn-Asn-Arg-Asp-Asn-Thr-Tyr-Asn-Arg-Val-
113 Iser-Glu-Asp-Leu-Arg-Ser-Arg-Ile-Glu-Val-
114 Iseu-Lys-Arg-Lys-Asn-Thr-Lys-Asn-Val-Arg-
115 Ala-Gln-Leu-Val-Asp-Met-Lys-Arg-Leu-Glu-
116 Ala-Gln-Leu-Val-Asp-Met-Lys-Arg-Leu-Glu-
117 Val-Asp-Ile-Lys-Ser-Tyr-Glu-Asp-Gln-His-
118 Arg-Gly-Ser-Clys-Ser-Arg-Asp-Arg-Gln-His-
119 Glu-Val-Asp-Leu-Ule-Lys-Met-Lys-Pro-Val-Pro-
120 Gln-Lys-Gln-Leu-Val-Pro-Gly-Asp-Arg-Gln-His-
121 Leu-Gln-Lys-Val-Pro-Gly-Asp-Arg-Gln-His-
122 Iseu-Pro-Leu-Val-Pro-Gly-Asp-Arg-Gln-His-
123 Iseu-Gly-Ser-Thr-Gly-Asp-Arg-Met-Glu-
125 Iseu-Thr-Asp-Met-Pro-Glu-Met-Arg-Met-Glu-
126 Iseu-Gly-Ser-Thr-Gly-Asp-Glu-Thr-Gly-
127 Ser-Gly-Ser-Thr-Gly-Ser-Ser-
138 Iser-Ala-Gly-Ser-Trp-Asn-Ser-Gly-
139 Gly-Pro-Gly-Ser-Trp-Asn-Ser-Gly-
130 Gly-Pro-Gly-Ser-Trp-Asn-Ser-Gly-
131 Ala-Gly-Ser-Trp-Asn-Ser-Gly-Ser-
132 Ala-Gly-Ser-Trp-Asn-Ser-Gly-Ser-
133 Ala-Gly-Ser-Trp-Asn-Ser-Gly-Ser-
134 Asp-Pro-Gly-Ser-Trp-Asn-Ser-Gly-
135 Ala-Gly-Ser-Trp-Asn-Ser-Gly-Ser-
136 Ala-Gly-Ser-Trp-Asn-Ser-Gly-
137 And Asp-New-Pro-Gly-Ser-
138 Asp-Pro-Gly-Ser-Thr-Gly-Ser-
139 Ala-Gly-Ser-Thr-Gly-Asn-Gly-
130 Ala-Gly-Ser-Thr-Gly-Asn-Ser-Gly-
131 Asp-Dro-Gly-Ser-Thr-Gly-Ser-Ser-Gly-
132 Asp-Pro-Gly-Ser-Thr-Gly-Ser-Ser-Gly-
133 Asp-Pro-Gly-Ser-Thr-Gly-Ser-Ser-Gly-
134 Asp-Pro-Gly-Ser-Thr-Gly-Ser-Thr-Gly-Ser-
135 Asp-Pro-Gly-Ser-Thr-Gly-Ser-
136 Asp-Pro-Gly-Ser-Thr-Gly-Ser-
137 Asp-Pro-Gly-Ser-Thr-Gly-Ser-
138 Asp-Pro-Gly-Ser-Thr-Gly-Ser-
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135 Asp-Pro-Gly-Ser-
136 Asp-Pro-Gly-
137 Asp-Pro-Gly-Ser-
138 Asp-Pr
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Asp-Ser-Gly-Glu-Gly-Asp-Pho-Leu-Ala-Glu-
Gly-Gly-Gly-Val-Arg-Gly-Pro-Arg-Val-Val-
Glu-Arg-His-Gln-Ser-Ala-Cys-Lys-Asp-Ser-
Asp-Trp-Pro-Pho-Cys-Ser-Asp-Glu-Asp-Trp-
Asp-Trp-Pro-Pho-Cys-Ser-Asp-Glu-Asp-Trp-
Ser-Pro-Arg-Pro-Gly-Ser-Thr-Gly-Thr-Trp-
Asn-Pro-Gly-Ser-Ser-Gl-Arg-Gly-Ser-Als-
Gly-His-Trp-Thr-Ser-Glu-Ser-Ser-Val-Ser-
Gly-Ser-Thr-Gly-Gln-Trp-His-Ser-Glu-Ser-
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n DGENE
; 35 D; 0 B; 9 C; 18 (; 20 F; 38 P; 91 S; 50)
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                                                                                                                                                                                                                              New hybrid proteins for use in tissue sealing and wound healing -
comprising a tissue-binding domain from a protein covalently linked to
crosslinking domain of another protein

N Irani M H
A (ZYMO) ZYMOGENETICS INC.
***WO 9416085 A2 19940721 87p***
I WO 1992-US12887 19931230
I WO 1992-US12887 19931230
RAI US 1992-998271 19921230
Patent
A English
S 1994-249231 [30]
PATENTS AQ070008
                                                                                                                                                    Fibronectin.

AAR60020 Protein
24 A; 42 R; 29 N;
33 L; 40 K; 12 M;
643
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AAR60020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 Gly-Ser-Phe-Arg-Pro-Asp-Ser-Pro-Gly-Ser-401 Gly-Ran-Alar-Arg-Pro-Asp-Ser-Pro-Asp-Trp-411 Gly-Thr-Phe-Glu-Glu-Val-Ser-Gly-Asp-Trp-421 Ser-Pro-Gly-Thr-Arg-Arg-Glu-Tyr-His-Thr-421 Glu-Lys-Leu-Val-Thr-Ser-Lys-Glu-Asp-Lys-441 Glu-Lys-Leu-Arg-Thr-Thr-Thr-Thr-Arg-Arg-Ser-441 Glu-Lys-Thr-Val-Thr-Thr-Thr-Arg-Arg-Ser-461 Glu-Val-Val-Thr-Yal-Thr-Thr-Thr-Arg-Arg-Ser-461 Glu-Val-Val-Thr-Ser-Glu-Asp-Gly-Ser-Asp-61 Glu-Val-Thr-Lys-Glu-Val-Thr-Lys-91 Cys-Pro-Gly-Thr-Leu-Asp-Gly-Ser-Asp-61 His-Arg-His-Pro-Asp-Glu-Ala-Ala-Phe-Pro-521 His-Arg-His-Pro-Asp-Glu-Ala-Ala-Phe-Pro-531 Gly-Phe-Phe-Thr-Gly-Lys-Thr-Phe-Pro-531 Gly-Phe-Phe-Thr-Asp-Glu-Ala-Ala-Phe-Pro-531 Gly-Phe-Phe-Thr-Ser-Pro-Gly-Lys-Thr-Phe-Phe-541 Val-Ser-Glu-Thr-Asp-Glu-Asa-Arg-Gly-Ser-His-Phe-Thr-Ser-Ser-Thr-Lys-Glu-Ser-551 Arg-Gly-Asp-Ser-Thr-Phe-Thr-Ser-Ser-Tyr-Asa-561 Ser-Gly-Asp-Ser-Thr-Phe-Glu-Ser-Ser-Tyr-Asa-591 Arg-Gly-Phe-Phe-Thr-Ser-Ser-Thr-Ser-Ser-Glu-Ser-Glu-Ser-Arg-Gly-Asp-Ser-Arg-Gly-Asp-Ser-Arg-Gly-His-Glu-Gly-Thr-His-Ser-Thr-Lys-Glu-Ser-Arg-Gly-His-Fla-Gly-Cyal-Arg-Gly-Lys-Pro-641 Ser-Leu-Ser-Pro-Leu-Gly-Lys-Pro-641 Ser-Leu-Ser-Pro-
                                                       Met-Phe-Ser-Met-Arg-Ile-Val-Cys-Leu-Val-
Leu-Ser-Val-Val-Gly-Thr-Ala-
Lep-Ser-Gly-Glu-Gly-Asp-Phe-Leu-Ala-Glu-
Asp-Ser-Gly-Val-Arg-Gly-Pro-Arg-Val-Val-
Gly-Gly-Val-Arg-Gly-Pro-Arg-Val-Val-
Glu-Arg-His-Gln-Ser-Ala-Cys-Lys-Asp-Ser-
                            Asp-Trp-Pro-Phe-Cys-Ser-Asp-Glu-Asp-Trp-
Asn-Tyr-Lys-Cys-Pro-Ser-Gly-Cys-Arg-Met-
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Lys-Met-Ala-Asp-Glu-Ala-Gly-Ser-Glu-Ala-Asp-His-Glu-Gly-Thr-His-Ser-Thr-Lys-Arg-Gly-His-Ala-Lys-Ser-Arg-Pro-Val-Arg-Gly-
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Leu-Glu-Arg-Pro-Gly-Gly-Asn-Glu-Ile-Thr-
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Ala-Gln-Leu-Val-Asp-Met-Lys-Arg-Leu-Glu-
Val-Asp-Ile-Asp-Ile-Lys-Ile-Arg-Ser-Cys-
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                                                                                                                                                              Gln-Phe-Thr-Ser-Ser-Thr-Ser-Tyr-Asn-Arg-
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                                                                                                                                                                                                                                                                                                                                                                                      ***DE 4242736
DE 1992-4242736
DE 1992-4242736
(FILE 'HOME' ENTERED AT 15:27:24 ON 07 OCT 2004)
                                                                                                                                                                                                                                                             1994-209452 [26]
Peptide corresponding to C-terminal fragment of cleaved fibrinogen.

AAR56269 peptide DGENE

AAR56269 peptide DGENE

L; 6 K; 1 M; 3 F; 2 P; 5 S; 1 T; 2 W; 2 Y; 1 V; 0 Others
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(BEHW) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR56269 peptide DGENE
Synthetic peptide(s) and antibodies against fragment E - derived plasmin-cleaved fibrinogen useful for therapy of disturbances in
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                                                                                                                                                                                                                                                                                                                                                                         Patent
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AAR56269 peptid
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31
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                                                                                                    Lys-Cys-Pro-Ser-Gly-Cys-Arg-Met-Lys-Gly-
Leu-Ile-Asp-Glu-Val-Asn-Gln-Asp-Phe-Thr-
Asn-Arg-Ile-Asn-Lys-Leu-Lys-Asn-Ser-Leu-
Phe-Glu-Tyr-Gln-Lys
                                                                                                                                                                           His-Gln-Ser-Ala-Cys-Lys-Asp-Ser-Asp-Trp-
Pro-Phe-Cys-Ser-Asp-Glu-Asp-Trp-Asn-Tyr-
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1 V; 0 Others
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334 DUP REM 11 (0 DUPLICATES REMOVED)
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FILE 'DGENE'

E' ENTERED AT 15:28:00 ON 07 OCT 2004
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641 HITS AT:

1 Leu-Ser-Pro 55-62

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=> s l1 L2

4 L1

=> s 12 and py<=2001 21560072 PY<=2001 L3 0 L2 AND PY<=2001 FULL ESTIMATED COST => log h COST IN U.S. DOLLARS SINCE FILE ENTRY 2.26

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TOTAL SESSION 29.39